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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the application of:

Aya Jakobovits, et al.

Serial No.:

10/001,469

Filing Date:

October 31, 2001

For:

NUCLEIC ACID AND CORRESPONDING

PROTEINS ENTITLED 101P3A11 **USEFUL IN TREATMENT AND**

DETECTION OF CANCER

Examiner: To be Assigned

Group Art Unit: 1642

AMENDMENT

Box Missing Parts Assistant Commissioner For Patents Washington, D.C. 20231

Dear Sir:

This is in response to the Notice to file missing parts of non-provisional application mailed December 20, 2001, for which a response is due on February 20, 2002. A petition for an extension of time of three (3) months until 20 May 2002 is attached hereto, along with the required fee.

Please enter the following sequence listing, amendments and remarks.

In the Specification

On page 1, line 26, please insert new paragraph as follows:

--SUBMISSION ON COMPACT DISC

The contents of the following submission on compact discs are incorporated herein by reference in its entirety: A compact disc copy of the Sequence Listing (COPY 1) (file name: 2002420, date recorded: February 16, 2002, size: 569 KB); a duplicate compact disc copy of Sequence Listing (COPY 2) (file name: 2002420, date recorded: February 16, 2002, size: 569 KB); a computer readable form copy of the Sequence Listing (CRF COPY) (file name: 2002420, date recorded: February 16, 2002, size: 569 KB).--

In the Sequence Listing

Please insert the attached compact disc copy of the Sequence Listing on CD-R (COPY 1) in the above-captioned application. A duplicate compact disc copy of the Sequence Listing on CD-R (COPY 2) and a computer readable form copy of the Sequence Listing on CD-R (CRF COPY) accompany this response.

AMENDMENTS

In the Specification:

Please replace the paragraph beginning at page 7, line 21, with the following rewritten paragraph:

-- Figure 1. 101P3A11 SSH sequence (SEQ ID NO:2960). The 101P3A11 SSH sequence.--

Please replace the paragraph beginning at page 7, line 22, with the following rewritten paragraph:

-- Figures 2A-2D. The cDNA (SEQ ID. NO. :2961) and amino acid sequence (SEQ ID. NO. :2962) of 101P3A11. The start methionine is underlined. The open reading frame extends from nucleic acid 133 to 1086 including the stop codon (the codon for the initial M is omitted as the shorter peptide has a more favorable Kozak sequence).--

Please replace the paragraph beginning at page 7, line 26, with the following rewritten paragraph:

--Figure 3. Amino acid sequence of 101P3A11 (SEQ ID. NO. :piece of 2962). The 101P3A11 protein has 317 amino acids.--

Please replace the paragraph beginning at page 7, line 28, with the following rewritten paragraph:

--Figure 4. Alignment of 101P3A11 (Sbjct) (SEQ ID NO: 2964) with mouse olfactory receptor S25 (Query.) (SEQ ID NO: 2963) The transmembrane regions of 101P3A11 and mouse olfactory receptor S25 (ORS25)predicted using the TMHMM algorithm are highlighted in gray. The amino acids of ORS25 predicted (Floriano, W.B., et al, 2000, Proc. Natl. Acad. Sci., USA, 97:10712-10716) to be involved in binding of the ligand hexanol and/or involved in the formation of the ligand binding pocket are italicized and bolded in the Figure, and are: Leu 131, Val 134, Val 135, Gly 138, Thr139, Ser 193, Ser 197, Phe 225, Ala 230, Ile 231, Gly 234, Thr 284, Phe 287, Gln 300, Lys 302.--

Please replace the paragraph beginning at page 11, line 31, with the following rewritten paragraph:

--Figure 23. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2965) with the rat (SEQ ID NO: 2966) GPCR RA1C (gi|3420759). Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%).--

Please replace the paragraph beginning at page 12, line 1, with the following rewritten paragraph:

--Figure 24. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2967) with the human prostate specific GPCR (SEQ ID NO: 2968) (gi|13540539). Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%).--

Please replace the paragraph beginning at page 12, line 3, with the following rewritten paragraph:

--Figure 25. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2969) with human olfactory receptor 5lI12, HOR5 (SEQ ID NO: 2970) (gi|14423836). Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%).--

Please replace the paragraph beginning at page 36, line 20, with the following rewritten paragraph:

--Also, different MHC class I molecules prefer a different length of ligands. For example, SYFPEITHI offers predictions for H2-Kb octamers, HLA-A*0201 nonamers and decamers, or HLA-B8 octamers and nonamers. The maximal scores vary between different MHC alleles. Therefore, one can include known ligands/epitopes in order to have an approximation of the scoring. For example, the maximal score for HLA-A*0201 peptides is 36. The well-known epitope GILGFVFTL (SEQ ID NO: 1401) derived from the influenza A matrix protein scores 30. All predicted MHC class II ligands are 15mers, consisting of three N-terminal flanking residues, the nonamer core sequence located within the binding groove, and three C-terminal flanking residues. Thus, anchor residue P1 appears in position 4 of the peptides predicted with "SYFPEITHI".--

Please replace the paragraph beginning at page 37, line 25, with the following rewritten paragraph:

--In an embodiment described in the examples that follow, 101P3A11 can be conveniently expressed in cells (such as 293T cells) transfected with a commercially available expression vector such as a CMV-driven expression vector encoding 101P3A11 with a C-terminal 6XHis (SEQ ID NO: 1402) and MYC tag (pcDNA3.1/mycHIS, Invitrogen or Tag5, GenHunter Corporation, Nashville TN). The Tag5 vector provides an IgGK secretion signal that can be used to facilitate the production of a secreted 101P3A11 protein in transfected cells. The secreted HIS-tagged 101P3A11 in the culture media can be purified, e.g., using a nickel column using standard techniques.--

Please replace the paragraph beginning at page 70, line 3, with the following rewritten paragraph:

--In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in a majority of a genetically diverse population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. Examples of such amino acid bind many HLA Class II molecules include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; (SEQ ID NO: 1403), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; (SEQ ID NO: 1404), and *Streptococcus* 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; (SEQ ID NO: 1405). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.--

Please replace the paragraph beginning at page 70, line 11, with the following rewritten paragraph:

--Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see*, *e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-

binding epitope peptide having the formula: aKXVAAWTLKAAa (SEQ ID NO: 1406), where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.--

Please replace the paragraph beginning at page 80, line 16, with the following rewritten paragraph:

--Single chain antibodies comprise the variable domains of the heavy and light chain joined by a flexible linker polypeptide, and are expressed as a single polypeptide. Optionally, single chain antibodies are expressed as a single chain variable region fragment joined to the light chain constant region. Well-known intracellular trafficking signals are engineered into recombinant polynucleotide vectors encoding such single chain antibodies in order to precisely target the intrabody to the desired intracellular compartment. For example, intrabodies targeted to the endoplasmic reticulum (ER) are engineered to incorporate a leader peptide and, optionally, a C-terminal ER retention signal, such as the KDEL (SEQ ID NO: 1407) amino acid motif. Intrabodies intended to exert activity in the nucleus are engineered to include a nuclear localization signal. Lipid moieties are joined to intrabodies in order to tether the intrabody to the cytosolic side of the plasma membrane. Intrabodies can also be targeted to exert function in the cytosol. For example, cytosolic intrabodies are used to sequester factors within the cytosol, thereby preventing them from being transported to their natural cellular destination.--

Please replace the paragraph beginning at page 86, line 29, with the following rewritten paragraph:

--pGEX Constructs: To generate recombinant 101P3A11 proteins in bacteria that are fused to the Glutathione S-transferase (GST) protein, all or parts of the 101P3A11 cDNA protein coding sequence are fused to the GST gene by cloning into pGEX-6P-1 or any other GST- fusion vector of the pGEX family (Amersham Pharmacia Biotech, Piscataway, NJ). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with GST fused at the amino-terminus and a six histidine epitope (6X His) (SEQ ID NO: 1402) at the carboxyl-

terminus. The GST and 6X His tags permit purification of the recombinant fusion protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-GST and anti-His antibodies. The 6X His tag (SEQ ID NO: 1402) is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the cloning primer at the 3' end, e.g., of the open reading frame (ORF). A proteolytic cleavage site, such as the PreScissionTM recognition site in pGEX-6P-1, can be employed that permits cleavage of the GST tag from 101P3A11-related protein. The ampicillin resistance gene and pBR322 origin permit selection and maintenance of the pGEX plasmids in *E. coli*. In one embodiment, amino acids 86-317 are cloned into the pGEX-2T expression vector, the protein is expressed and purified.--

Please replace the paragraph beginning at page 87, line 8, with the following rewritten paragraph:

--pMAL Constructs: To generate, in bacteria, recombinant 101P3A11 proteins that are fused to maltose-binding protein (MBP), all or parts of the 101P3A11 cDNA protein coding sequence are fused to the MBP gene by cloning into the pMAL-c2X and pMAL-p2X vectors (New England Biolabs, Beverly, MA). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with MBP fused at the amino-terminus and a 6X His (SEQ ID NO: 1402) epitope tag at the carboxyl-terminus. The MBP and 6X His tags (SEQ ID NO: 1402) permit purification of the recombinant protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-MBP and anti-His antibodies. The 6X His (SEQ ID NO: 1402) epitope tag is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the 3' cloning primer. A Factor Xa recognition site permits cleavage of the pMAL tag from 101P3A11. The pMAL-c2X and pMAL-p2X vectors are optimized to express the recombinant protein in the cytoplasm or periplasm respectively. Periplasm expression enhances folding of proteins with disulfide bonds. In one embodiment, amino acids 86-310 is cloned into the pMAL-c2X expression vector, the protein is expressed and purified.--

Please replace the paragraph beginning at page 87, line 20, with the following rewritten paragraph:

--pET Constructs: To express 101P3A11 in bacterial cells, all or parts of the 101P3A11 cDNA protein coding sequence are cloned into the pET family of vectors (Novagen, Madison, WI). These vectors allow tightly controlled expression of recombinant 101P3A11 protein in bacteria with and without fusion to proteins that enhance solubility, such as NusA and thioredoxin (Trx), and epitope tags, such as 6X His (SEQ ID NO: 1402) and S-Tag ™ that aid purification and detection of the recombinant protein. For example, constructs are made utilizing pET NusA fusion system 43.1 such that regions of the 101P3A11 protein are expressed as amino-terminal fusions to NusA.--

Please replace the paragraph beginning at page 88, line 19, with the following rewritten paragraph:

--pcDNA4/HisMax Constructs: To express 101P3A11 in mammalian cells, the 101P3A11 ORF was cloned into pcDNA4/HisMax Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter and the SP16 translational enhancer. The recombinant protein has XpressTM and six histidine (6X His) (SEQ ID NO: 1402) epitopes fused to the amino-terminus. The pcDNA4/HisMax vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Zeocin resistance gene allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and CoIE1 origin permits selection and maintenance of the plasmid in *E. coli.*--

Please replace the paragraph beginning at page 88, line 28, with the following rewritten paragraph:

--pcDNA3.1/MycHis Constructs: To express 101P3A11 in mammalian cells, the 101P3A11 ORF, with a consensus Kozak translation initiation site, was cloned into pcDNA3.1/MycHis Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the myc epitope and 6X His (SEQ ID NO: 1402) epitope fused to the carboxyl-terminus. The pcDNA3.1/MycHis vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability, along with the SV40 origin for episomal replication and

simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene can be used, as it allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli.*—

Please replace the paragraph beginning at page 89, line 16, with the following rewritten paragraph:

--PAPtag: The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pAPtag-5 (GenHunter Corp. Nashville, TN). This construct generates an alkaline phosphatase fusion at the carboxyl-terminus of the 101P3A11 proteins while fusing the IgGκ signal sequence to the amino-terminus. Constructs are also generated in which alkaline phosphatase with an amino-terminal IgGκ signal sequence is fused to the amino-terminus of 101P3A11 proteins. The resulting recombinant 101P3A11 proteins are optimized for secretion into the media of transfected mammalian cells and can be used to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter and the recombinant proteins also contain myc and 6X His (SEQ ID NO: 1402) epitopes fused at the carboxyl-terminus that facilitates detection and purification. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the recombinant protein and the ampicillin resistance gene permits selection of the plasmid in *E. coli.*--

Please replace the paragraph beginning at page 89, line 27, with the following rewritten paragraph:

--ptag5: The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pTag-5. This vector is similar to pAPtag but without the alkaline phosphatase fusion. This construct generated 101P3A11 protein with an amino-terminal IgGκ signal sequence and myc and 6X His (SEQ ID NO: 1402) epitope tags at the carboxyl-terminus that facilitate detection and affinity purification. The resulting recombinant 101P3A11 protein was optimized for secretion into the media of transfected mammalian cells, and was used as immunogen or ligand to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter. The Zeocin resistance gene present in the vector allows for

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selection of mammalian cells expressing the protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli.*--

Please replace the paragraph beginning at page 90, line 30, with the following rewritten paragraph:

--Additional pSRα constructs are made that fuse an epitope tag such as the FLAGTM tag to the carboxyl-terminus of 101P3A11 sequences to allow detection using anti-Flag antibodies. For example, the FLAGTM sequence 5' gat tac aag gat gac gat aag 3' (SEQ ID NO: 1408) is added to cloning primer at the 3' end of the ORF. Additional pSRα constructs are made to produce both amino-terminal and carboxyl-terminal GFP and myc/6X His (SEQ ID NO: 1402) fusion proteins of the full-length 101P3A11 proteins.--

Please replace the paragraph beginning at page 141, line 31, with the following rewritten paragraph:

--The generation of anti-101P3A11 polyclonal Ab (pAb) using an amino-terminal peptide encoding amino acids 1-14 (MVDPNGNESSATYF; (SEQ ID NO: 1409) as antigen was reported in our Priority Application. The effect of this antibody on 101P3A11 mediated ERK phosphorylation (Figure 38) and cAMP accumulation (Figure 39) was determined. 293T cells were transfected with control or 101P3A11 cDNA. Cells were allowed to rest overnight, and treated with anti-101P3A11 or control Ab in the presence of 0.5% or 10% FBS. Cells were lysed and analyzed by Western blotting with anti-Phospho-ERK and anti-ERK mAb. Figure 38 shows that expression of 101P3A11 induces ERK phosphorylation in cells treated with 0.5 or 10% FBS. Anti-101P3A11 pAb reduced the phosphorylation of ERK in 293T-101P3A11 cells treated with 0.5% FBS. The ERK overlay demonstrated equal loading, supporting the specificity of this data.--

Please replace Table XIX, beginning at page 186, with the following rewritten Table XIX:

-- Table XIX: Motifs and Post-translational Modifications of 101P3A11

N-glycosylation site

Number of matches: 3

- 7-10 NESS (SEQ ID NO: 1410)
- 2 44-47 NLTI (SEQ ID NO: 1411)
- 90-93 NSTT (SEQ ID NO: 1412)



cAMP- and cGMP-dependent protein kinase phosphorylation site 268-271 RRDS (SEQ ID NO: 1413)

Protein kinase C phosphorylation site 266-268 SKR

Casein kinase II phosphorylation site Number of matches: 3

- 56-59 SLHE (SEQ ID NO: 1414) 69-72 SGID (SEQ ID NO: 1415)
- 110-113 SGME (SEQ ID NO: 1416)

N-myristoylation site

Number of matches: 4

- 6-11 GNESSA (SEQ ID NO: 1417)
- 2 21-26 GLEEAQ (SEQ ID NO: 1418) 3 111-116 GMESTV (SEQ ID NO: 1419) 4 240-245 GTCVSH (SEQ ID NO: 1420)

G-protein coupled receptors family 1 signature

112-128 MESTVLLAMAFDRYVAI (SEQ ID NO: 1421)--

Please replace Table XXI, beginning at page 190, line 1, with the following rewritten Table XXI:

--Table XXI: Nucleotide sequence of the splice variant (SEQ ID NO: 1422)

1	CACATTCCTT	CCATACGGTT	GAGCCTCTAC	CTGCCTGGTG	CTGGTCACAG	TTCAGCTTCT
61	TCATGATGGT	GGATCCCAAT	GGCAATGAAT	CCAGTGCTAC	ATACTTCATC	CTAATAGGCC
121	TCCCTGGTTT	AGAAGAGGCT	CAGTTCTGGT	TGGCCTCCCA	TTGTGCTCCC	TCTANCTATG
181	CTGTGCTAGT	AATTGACAAT	CATCTACATG	TGCGGACGAG	CACGNCGCNG	AGCCCNGTAT
241	NATTCTGCNG	CTTCAGCATG	ACACCCTNCA	GTCTCAGCCA	AAGNGCATCT	CNGTCAATCA
301	NACACNTGAG	CTGTCGTACG	AGTTGCATCA	TCCTANGGCA	GGATCAATGT	GCGGNAGGCN
361	TGACGCAGTG	CACGTACCAT	GGCAGCAAGA	CAGGGCCGGT	ACAAATGGGG	GCGAGNCGGG
421	GTGAAGATGN	ACCCTCGGGT	CANAGAGTGC	CTCTGCGCCA	AAACCTCCAT	CATGNNAACA
481	GNGTATAACG	GCGNAGAATC	GGNNANGCGC	AAGGCTAAGG	AAANNCCCAA	NNCNGGTACT
541	TTAACCCNGC	AAANGGCANC	NAAACGGGNG	GGTNANTGAA	CAAGGAAGGN	NTGNAACTGG
601	GCCAAAACGG	GNTGGGCAAN	NNAAGGACTC	ATGGGNCCAA	GGGACGGNAA	AAGGGGNAAN
661	CGGGGCGAAA	TGNNAAAAAC	CGGGNCCCGG	GGAANAANGA	AGGGGAANAN	GNGTGAAGGA
721	CNGGGTTCAA	GGGAAAAGNA	AAACCANGGG	NNAGAAACCN	TTCNAANGGC	CCGGGNANGA

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781 AAGGAANTNN GNNNGGNGAA AAAATCNAAA AAAAGCNGNG GCNNAAAAAN GGGGGGAANN
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- 841 NAAANACCNN GGNCGNNAAA AAACNNAANG NGGGGGGANT ANACACGGAA ANNNANGGGC
- 901 GNNNAAGGGA AATAANNCGG GAACNAAAGN GCAAACCGNA CGGNAGGAAC GAAACCCACC
- 961 GGAGNCGCNN AACGCCNNNC NNANCCCGAG CNGAGGTNG--

Please replace Table XXII, beginning at page 190, line 38, with the following rewritten Table XXII:

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-Table XXII: Nucleotide sequence alignment of 101P3A11 with the splice variant.
```

```
Score = 337 bits (175), Expect = 4e-89
Identities = 215/223 (96%), Gaps = 6/223 (2%)
Strand = Plus / Plus
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101P3A11: 68 cacattccttccatacggttgagcctctacctgcctggtgctggtcacagttcagcttct 127 (SEQ ID NO: 1423)

Variant : 1 cacattccttccatacggttgagcctctacctgcctggtgctggtcacagttcagcttct 60 (SEQ ID NO: 1424)
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Please replace Table XXIII, beginning at page 191, line 8, with the following rewritten Table XXIII:

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--Table XXIII: Longest single amino acid sequence alignment of 101P3A11 and the splice variant.
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Score = 134 bits (287), Expect(2) = 3e-29
Identities = 51/51 (100%)
Frame = +1 / +3
```

101P3A11: 70 HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 222 (SEQ ID NO: 1425)

HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA
Variant: 3 HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 155
(SEQ ID NO: 1426)--

Please replace Table XXIV, beginning at page 191, line 16, with the following rewritten Table XXIV:

--Table XXIV: Peptide sequences from the translation of the nucleotide sequence of the splice variant .

	Sprice varianc.
Open reading	Amino acid sequences
frame	
Frame 1 (SEQ ID	HIPSIRLSLYLPGAGHSSASS*WWIPMAMNPVLHTSS**ASLV*KRLSSGWPPIVLPLXM
NO: 1427)	LC**LTIIYMCGRARRXAXYXSAASA*HPXVSAKXHLXQSXT*AVVRVASSXGRINVRXA
	*RSARTMAARQGRYKWGRXGVKMXPRVXECLCAKTSIMXTXYNGXESXXRKAKEXPXXGT
	LTXQXAXKRXGX*TRKXXNWAKTGWAXXGLMGPRDGKRGXRGEMXKTGXRGXXKGXXXEG
	XGSREKXNXGXETXXXARXXKEXXXXKKSKKSXGXKXGGXXXPXXXKNXXXGXXTRKXXG
	XXGK*XGNXXANRTXGTKPTGXAXRXXXPEXRX
Frame 2(SEQ ID	TFLPYG*ASTCLVLVTVQLLHDGGSQWQ*IQCYILHPNRPPWFRRGSVLVGLPLCSLXLC
NO: 1428)	CASN*QSSTCADEHXAEPXXILXLQHDTLQSQPKXISVNXTXELSYELHHPXAGSMCGRX
	DAVHVPWQQDRAGTNGGEXG*RXTLGSXSASAPKPPSXXQXITAXNRXXARLRKXPXXVL
	*PXKXXXNGXVXEQGRXXTGPKRXGQXKDSWXQGTXKGXXGAKXXKPGPGEXXRGXXVKD
	XVQGKXKTXGXKPFXXPGXERXXXXXKNXKKAXAXKXGEXKXXGRXKTXXGGXXHGXXXA
	XKGNXXGTKXQTXRXERNPPEXXNAXXXPSXG
Frame 3(SEQ ID	HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLASHCAPSXYA
NO: 1429)	VLVIDNHLHVRTSTXXSPVXFCXFSMTPXSLSQXASXSIXHXSCRTSCIILXQDQCAXGX
1	TQCTYHGSKTGPVQMGAXRGEDXPSGXRVPLRQNLHHXNXV*RRRIGXAQG*GXXQXXYF
	NPAXGXXTGGXXNKEGXXLGQNGXGXXRTHGXKGRXKGXXGRNXKNRXPGXXEGEXX*RT
	GFKGKXKPXXRNXSXGPGXKGXXXGEKIXKKXXXKXGGXXXTXXXKKXXXGGXXTEXXGR
	XREIXREXKXKPXGRNETHRXRXTPXXXRAEV

Note: Frame 3 gives the longest subsequence that is identical with 101P3All amino acid sequence. In this Table each (*)indicates the product of a single stop codon, and 'X' indicates a single unknown amino acid.--

Please replace Table XXVI, beginning at page 193, line 1, with the following rewritten Table XXVI:

--Table XXVI:

HLA Class I Nonamers (SEQ ID NOS 1430-1462, respectively in order of appearance)

HLA-A1 nonomers														
	Pos 1 2 3 4 5 6 7 8 9 s													
1	245	Н	v	C	Α	V	F	I	F	Y	24			
2	29	\mathbf{L}	A	F	P	L	C	$\underline{\underline{s}}$	L	Y	21			
3	41	V	L	G	N	L	T	I	I	Y	21			
4	285	P	P	v	L	N	P	Ī	V	Y	20			
5	111	G	M	E	S	Т	V	$\underline{\mathbf{L}}$	L	Α	19			
6	117	L	$\overline{\Gamma}$	A	М	Α	F	$\underline{\underline{D}}$	R	Y	19			
7	172	R	$\underline{\mathbf{s}}$	N	1	L	S	$\overline{\mathbf{H}}$	S	Y	19			
8	192	D	$\overline{\mathbf{D}}$	I	R	V	N	V	V	Y	19			
9	212	D	s	L	\mathbf{L}	I	S	$\underline{\mathbf{F}}$	S	Y	19			
10	57	L	H	E	P	М	Y	Ī	F	L	18			
11	22	L	E	E	A	Q	F	W	L	A	17			
12	9	s	\underline{s}	A	T	Y	F	<u>I</u>	L	I	16			
13	52	R	$\underline{\underline{T}}$	E	Н	S	L	H	E	P	16			

	HLA-A1	nc	nc	me	ers						
	Pos	1	2	3	4	5	6	7	8	9	score
14	54	E	\overline{H}	s	\mathbf{L}	Н	E	P	Μ	Y	16
15	78	S	$\underline{\mathbf{s}}$	M	P	K	М	$\underline{\mathbf{L}}$	Α	I	16
16	95	Q	\mathbf{F}	D	А	С	L	Ŀ	Q	I	16
17	159	Α	<u>P</u>	L	P	V	F	Ī	K	Q	16
18	183	Н	Q	D	V	М	K	$\underline{\underline{\mathbf{r}}}$	Α	С	16
19	1	М	V	D	P	N	G	$\underline{\mathbf{N}}$	E	s	15
20	5	N	G	N	E	S	S	A	T	Y	15
21	210	G	Ī	D	S	\mathbf{r}	L	I	s	F	15
22	273	L	<u>P</u>	v	I	L	Α	N	I	Y	15
23	271	S	$\underline{\mathbf{P}}$	L	P	V	Ι	$\overline{\Gamma}$	Α	N	14
24	91	S	$\underline{\mathbf{T}}$	T	I	Q	F	$\underline{\mathtt{D}}$	Α	С	13
25	121	Α	F	D	R	Y	V	A	1	С	13
26	138	L	T	L	P	R	V	$\underline{\underline{\mathbf{T}}}$	K	I	13
27	218	F	S	Y	L	\mathbf{L}	I	$\overline{\mathbf{r}}$	K	T	13
28	282	L	$\overline{\mathbf{r}}$	V	P	P	V	L	N	P	13
29	190	Α	$\underline{\underline{C}}$	D	D	Ι	R	$\overline{\Lambda}$	N	v	12
30	191	C	$\overline{\mathbf{D}}$	D	Ι	R	٧	$\underline{\mathbf{N}}$	V	v	12
31	231	Т	R	E	Α	Q	Α	K	Α	F	12
32	268	R	R	D	S	P	L	P	V	I	12
33	270	D	<u>s</u>	P	L	P	V	Ī	L	A	12

HLA-A*0201 nonomers(SEQ ID NOS 1463-1569, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	287	v	L	N	P	I	v	Y	G	v	30
2	14	F	I	L	1	G	L	P	G	L	29
3	28	W	L	Α	F	P	L	С	S	L	28
4	37	Y	L	Ι	Α	V	$\overline{\Gamma}$	G	N	L	28
5	222	L	I	L	K	Т	V	L	G	L	28
6	66	C	M	L	S	G	Ī	D	Ι	L	26
7	108	S	L	S	G	М	$\underline{\mathtt{E}}$	S	T	V	26
8	181	С	L	Н	Q	D	$\overline{\Lambda}$	M	K	L	26
9	201	G	L	I	V	Ι	$\underline{\mathtt{I}}$	S	A	I	26
10	214	L	L	Ι	S	F	$\underline{\underline{s}}$	Y	L	L	26
11	275	V	I	L	Α	N	Ī	Y	L	L	26
12	157	L	M	A	P	L	<u>P</u>	V	F	I	25
13	220	Y	L	L	Ι	L	K	T	V	L	25
14	276	I	L	Α	N	Ι	$\underline{\underline{Y}}$	L	L	V	25
15	279	N	I	Y	\mathbf{L}	L	\underline{v}	P	P	v	25
16	138	L	T	L	Ρ	R	$\underline{\mathtt{v}}$	T	K	I	24
17	213	S	L	L	Ι	S	F	S	Y	L	24
18	49	Y	I	V	R	T	$\underline{\mathbf{E}}$	Η	S	L	23
19	143	V	T	K	Ι	G	\underline{v}	A	A	v	23
20	188	K	L	Α	C	D	$\underline{\mathtt{D}}$	Ι	R	v	23
21	198	V	v	Y	G	L	I	V	Ι	I	23
22	21	G	L	E	E	A	\underline{Q}	F	W	L	22
23	40	A	V	L	G	N	$\overline{\Gamma}$	T	Ι	I	22
24	206	I	s	Α	Ι	G	$\overline{\Gamma}$	D	S	L	22
25	11	Α	T	Y	F	1	$\underline{\mathbf{L}}$	Ι	G	L	21
26	60	P	M	Y	I	F	$\overline{\Gamma}$	C	M	L	21
											14

HLA-A*0201 nonomers (SEQ ID NOS 1463-1569, respectively in order of appearance)

				-	•						
	Pos	1	2	3	4	5	6	7	8	9	score
27	135	A	T	v	L	T	L	P	R	v	21
28	160	P	L	P	v	F	Ξ	ĸ	Q	L	21
29	174	N	I	L	s	Н	÷ S	Y	C	L	21
30	207	s	A	I	G	L	D D	s	L	L	21
31	272	P	L	P	v	I	L	A	И	I	21
32	283	L	v	P	P	v	L	N	P	I	21
33	67	М	L	S	G	I	D	I	L	I	20
34	101	L	Õ	I	F	A	ī	H	S	L	20
35	282	L	L	V	P	P	v	ь	И	P	20
36	299	E	I	v R				Г	R		20
		I			Q T	R	I			L	
37	304		L A	R V	L	F	H	V	A	T	20
38	39	I	Т		L	G	<u>n</u>	L	T	I	19
39	45	L		I		Y	Ī	V	R	T	19
40	92	T	T	I	Q	F	D	A	C	L	19
41	110	S	G	M	E	S	T	V	L	L	19
42	127	A	I	C	Н	P	<u>r</u>	R	Н	A	19
43	132	L	R	Н	A	T	v	L	T	L	19
44	149	A	A	V	V	R	<u>G</u>	A	A -	L	19
45	155	A	A	L	M	A	<u>P</u>	L	P	V	19
46	156	A	L	M	Α	P	ī	Р	V	F	19
47	203	1	V	Ι	Ι	S	<u>A</u>	Ι	G	L	19
48	208	A	I	G	L	D	<u>s</u>	L	L	Ι	19
49	216	Ι	S	F	S	Y	$\overline{\Gamma}$	L	I	L	19
50	219	S	Y	L	L	Ι	ഥ	к	T	v	19
51	221	L	L	Ι	L	K	T	V	L	G	19
52	223	1	L	K	Т	V	Ē	G	L	Т	19
53	17	I	G	\mathbf{L}	Р	G	Ë	E	E	Α	18
54	33	L	С	S	L	Y	$\overline{\mathbf{r}}$	Ι	A	V	18
55	34	С	s	L	Y	L	<u>T</u>	A	V	L	18
56	38	\mathbf{L}	Ι	A	V	L	$\underline{\mathbf{G}}$	N	L	Т	18
57	43	G	N	L	Т	Ι	I	Y	Ι	v	18
58	85	Α	Ι	F	W	F	$\overline{\mathbf{N}}$	S	Т	T	18
59	118	L	Α	M	A	F	$\overline{\mathbf{D}}$	R	Y	v	18
60	194	Ι	R	٧	N	V	V	Y	G	L	18
61	210	G	L	D	S	L	$\overline{\mathbf{r}}$	Ι	S	F	18
62	215	\mathbf{L}	I	S	F	S	$\underline{\mathbf{Y}}$	L	L	Ι	18
63	246	V	С	A	V	F	Ī	F	Y	v	18
64	254	V	P	F	Ι	G	Ī	s	M	v	18
65	15	I	L	Ι	G	L	<u>P</u>	G	L	E	17
66	63	I	F	L	C	M	$\overline{\mathbf{r}}$	S	G	I	17
67	72	D	I	L	Ι	S	$\underline{\mathbf{T}}$	S	S	M	17
68	93	\mathbf{T}	I	Q	F	D	$\underline{\underline{\mathbf{A}}}$	C	L	L	17
69	98	Α	C	L	\mathbf{L}	Q	<u>I</u>	F	A	I	17
70	111	G	М	E	S	Т	$\underline{\mathtt{v}}$	\mathbf{L}	L	A	17
71	120	М	A	F	D	R	$\underline{\underline{Y}}$	V	Α	I	17
72	167	Q	L	P	F	C	R	s	N	I	17
73	197	N	V	V	Y	G	Ē	Ι	٧	I	17
74	226	T	v	L	G	L	$\underline{\mathbf{T}}$	R	E	A	17
75	281	Y	L	L	٧	P	P	V	L	N	17
											15

HLA-A*0201 nonomers(SEQ ID NOS 1463-1569, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
76	31	F	P	L	С	s	L	Y	L	I	16
77	56	S	L	Н	E	P	M	Y	Ι	F	16
78	70	G	I	D	Ι	L	ī	S	Т	s	16
79	78	s	S	М	P	K	M	L	Α	I	16
80	79	s	M	P	K	М	L	A	Ι	F	16
81	104	F	A	I	Н	S	Ļ	S	G	M	16
82	119	Α	M	Α	F	D	R	Y	V	A	16
83	144	Т	K	Ι	G	V	A	A	V	v	16
84	147	G	v	Α	A	V	V	R	G	A	16
85	186	V	M	K	L	Α	<u>C</u>	D	D	I	16
86	230	L	T	R	Ε	Α	$\underline{{\sf Q}}$	Α	K	A	16
87	238	Α	F	G	\mathbf{T}	C	V	S	Н	v	16
88	249	V	F	Ι	F	Y	$\overline{\Lambda}$	P	F	Ι	16
89	302	Q	R	Ι	L	R	$\bar{\overline{\Gamma}}$	F	Н	V	16
90	303	R	I	L	R	L	$\underline{\mathbf{F}}$	Н	V	A	16
91	18	G	L	P	G	L	$\underline{\mathbf{E}}$	E	A	Q	15
92	35	S	L	Y	L	Ι	A	V	L	G	15
93	42	L	G	N	L	Т	Ī	Ι	Y	I	15
94	46	Т	I	Ι	Y	Ι	<u>v</u>	R	T	Е	15
95	69	S	G	Ι	D	Ι	$\overline{\Gamma}$	Ι	S	T	15
96	76	S	T	S	S	M	P	K	M	L	15
97	131	P	L	R	Н	A	$\underline{\mathtt{T}}$	V	L	T	15
98	137	V	L	Т	L	P	\underline{R}	V	T	K	15
99	153	R	G	A	A	L	\underline{M}	A	P	L	15
100	190	Α	С	D	D	Ι	\underline{R}	V	N	V	15
101	191	C	D	D	Ι	R	\underline{V}	N	V	V	15
102	204	V	I	Ι	S	A	Ī	G	L	D	15
103	241	\mathbf{T}	С	V	S	Η	$\overline{\Lambda}$	С	A	V	15
104	251	I	F	Y	V	P	F	Ι	G	L	15
105	269	R	D	S	P	L	P	V	Ι	L	15
106	280	Ι	Y	L	L	V	<u>P</u>	Þ	V	L	15
107	306	R	L	F	Η	V	<u>A</u>	Т	Н	A	15

HLA A*0203 nonomers (SEQ ID NOS 1570-1594, respectively in order of appearance)

	Pos	,	2	2		_	_	7	0	^	score
		1	2	3	4	5	0	,	В	9	
1	148	V	$\underline{\underline{\mathbf{A}}}$	A	V	V	R	$\underline{\mathbf{G}}$	Α	A	14
2	119	Α	$\underline{\underline{M}}$	A	\mathbf{F}	D	R	Y	V	A	13
3	147	G	\underline{v}	A	Α	V	V	$\underline{\mathbf{R}}$	G	A	12
4	97	D	A	C	L	L	Q	I	F	A	11
5	127	Α	I	C	Н	P	L	R	Н	A	10
6	3	D	<u>P</u>	N	G	N	E	<u>s</u>	S	A	9
7	17	I	G	L	P	G	L	$\underline{\mathbf{E}}$	Ε	A	9
8	22	L	E	E	A	Q	F	\overline{M}	L	A	9
9	32	P	$\underline{\mathbf{L}}$	С	S	L	Y	$\overline{\mathbf{r}}$	Ι	A	9
10	77	T	\underline{s}	S	М	P	K	$\underline{\underline{M}}$	L	A	9
11	90	N	$\underline{\mathbf{s}}$	T	T	I	Q	$\underline{\mathbf{F}}$	D	A	9
											16

HLA A*0203 nonomers (SEQ ID NOS 1570-1594, respectively in order of appearance)

1 2 3 4 5 6 7 8 9 12 111	9
13 113 E S T V L L A M A 14 141 P R V T K I G V A 15 142 R V T K I G V A A 16 151 V V R G A A L M A 17 182 L H Q D V M K L A 18 200 Y G L I V I I S A 19 226 T V L G L T R E A	_
14 141 P R V T K I G V A 15 142 R V T K I G V A A 16 151 V V R G A A L M A 17 182 L H Q D V M K L A 18 200 Y G L I V I I S A 19 226 T V L G L T R E A	
15 142 R V T K I G V A A 16 151 V V R G A A L M A 17 182 L H Q D V M K L A 18 200 Y G L I V I I S A 19 226 T V L G L T R E A	9
16 151 V V R G A A L M A 17 182 L H Q D V M K L A 18 200 Y G L I V I I S A 19 226 T V L G L T R E A	9
17 182 L H Q D V M K L A 18 200 Y G L I V I I S A 19 226 T V L G L T R E A	9
18 200 Y $\frac{G}{L}$ L V I $\frac{I}{L}$ S A 19 226 T $\frac{V}{L}$ L G L T $\frac{R}{L}$ E A	9
19 226 T $\underline{\underline{V}}$ L G L T $\underline{\underline{R}}$ E A	9
	9
20 228 L G L T R E A Q A	9
	9
21 230 L <u>T</u> R E A Q <u>A</u> K A	9
22 240 G <u>T</u> C V S H <u>V</u> C A	9
23 270 D S P L P V I L A	9
24 303 R <u>I</u> L R L F <u>H</u> V A	9
25 306 R <u>L</u> F H V A <u>T</u> H A	9

<u>HLA-A26</u> nonomers (SEQ ID NOS 1595-1675, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	R	Q	R	I	L	R	L	30
2	72	D	Ι	L	Ι	s	Т	S	s	M	27
3	248	А	V	F	I	F	Y	V	Р	F	27
4	210	G	L	D	s	L	L	I	s	F	.26
5	14	F	I	L	Ι	G	L	P	G	L	24
6	56	S	L	Н	E	P	М	Y	r	F	24
7	117	L	L	Α	М	Α	F	D	R	Y	24
8	222	L	Ι	L	K	Т	V	L	G	L	24
9	245	Н	V	C	Α	V	F	1	F	Y	24
10	11	Α	T	Y	F	Ι	L	I	G	\mathbf{L}	23
11	37	Y	L	Ι	Α	V	L	G	N	L	23
12	114	S	T	V	${f L}$	L	A	М	Α	F	23
13	156	Α	L	M	Α	P	L	P	٧	F	23
14	162	P	V	F	I	K	Q	L	P	F	23
15	181	C	L	Н	Q	D	V	M	K	L	23
16	28	W	L	Α	F	P	L	С	S	L	22
17	92	\mathbf{T}	\mathbf{T}	Ι	Q	F	D	Α	C	L	22
18	160	P	\mathbf{L}	Ρ	V	F	Ι	K	Q	\mathbf{L}	22
19	203	I	V	Ι	Ι	s	Α	Ι	G	L	22
20	213	S	L	L	Ι	S	F	s	Y	L	22
21	275	V	Ι	L	Α	N	Ι	Y	L	L	22
22	193	D	Ι	R	V	N	V	V	Y	G	21
23	242	C	V	S	Н	V	C	A	V	F	21
24	76	S	T	S	S	M	P	K	М	L	20
25	253	Y	V	P	F	I	G	L	S	М	20
26	274	P	V	Ι	L	Α	И	I	Y	\mathbf{L}	20
27	23	E	E	A	Q	F	W	L	A	F	19
28	41	V	L	G	N	L	Т	Ι	I	Y	19
29	49	Y	I	V	R	Т	E	Η	S	L	19
											17

 $\underline{\underline{\text{HLA-A26}}}$ nonomers (SEQ ID NOS 1595-1675, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
30	150	A	V	V	R	G	A	A	L	M	19
31	174	N	I	ь Г	s	Н	S	Y	С	L	19
32	192	D	D	I	R	V	И	v	v	Y	19
33	214	L	L	I	S	F	S	Y	L	L	19
34	251	1	F	Y	V	Р	F	I	G	L	19
35	251 8	E	S	S	A	T	Y	F	I	L	18
36	21	G	L	E	E	A	Q	F	M	L	18
37		L	Т	I	I	Y	I	v	R	Т	18
	45 54	E	Н	S	L	Н	E	v P	M	Y	18
38			н Р	М	Y	I					
39	59	E					F	L	C	M	18
40	88	W	F	N	S	T	T	I	Q	F	18
41	93	T	I	Q	F	D	A	C	L	Г	18
42	185	D		M	K	L	A	C	D	D	18
43	198	٧	V	Y	G	L	I	V	I	I	18
44	62	Y	I	F	L	C	M	L	S	G	17
45	70	G	I	D	I	L	Ι	S	T	S	17
46	79	S	M	P	K	M	L	A	I	F	17
47	96	F	D	A	C	L	L	Q	I	F	17
48	104	F	A	Ι	Н	S	L	S	G	M	17
49	138	L	T	L	P	R	v	Т	K	1	17
50	143	V	T	K	I	G	v	A	A	V	17
51	204	V	I	1	s	A -	I	G	L	D	17
52	212	D	S	L	L	Ι	S	F	S	Y	17
53	220	Y	L	L	I	L	K	Т	V	L	17
54	256	F	Ι	G	L	S	M	V	H	R	17
55	283	L	V	P	P	V	L	N	P	Ι	17
56	29	L	A	F	P	L	C	s	L	Y	16
57	40	A	V	L	G	N	L	T	I	I	16
58	46	Т	I	I	Y	I	V	R	Т	E	16
59	52	R	T	E	Н	S	L	H	E	P	16
60	75	I	S	Т	S	S	M	P	K	M	16
61	91	S	Т	Т	I	Q	F	D	A	С	16
62	135	A	T	V	Ь	Т	L	P	R	V	16
63	147	G	V	A	A	V	V	R	G	A	16
64	201	G	L	1	V	I	I	S	A	I	16
65	257	I	G	L	s	M	V	Н	R	F	16
66	279	N	I	Y	L	L	V	P	P	V	16
67	30	A	F	P	L	C	S	L	Y	L	15
68	101	L	Q	I	F	A	Ι	Н	S	L	15
69	115	Т	V	L	L	A	M	A	F	D	15
70	127	A	I	C	Η	Ρ	L	R	H	A	15
71	153	R	G	A	A	L	M	A	P	L	15
72	163	v	F	Ι	K	Q	L	P	F	C	15
73	215	L	I	S	F	S	Y	L	L	Ι	15
74	216	I	S	F	S	Y	L	L	Ι	L	15
75	225	K	Т	V	L	G -	L	Т	R	E	15
76	272	P -	L	P	V	Ι	L	A	N	I	15
77	282	L	L	V	P	P	V	L	N	P	15
78	286	P	V	L	N	P	Ι	V	Y	G	15
											18

$\overline{\text{HLA-A26}}$ nonomers (SEQ ID NOS 1595-1675, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
79	287	V	L	N	P	Ι	V	Y	G	V	15
80	296	K	Т	K	E	Ι	R	Q	R	Ι	15
81	303	Ð	т	Τ.	R	т.	F	н	37	Δ	15

HLA-A3 nonomers(SEQ ID NOS 1676-1747, respectively in order of appearance)

	Pos		2	3	4	5	_	7	8	9	score
1	137	1 V	L	3 T	4 L	5 P	6 R	v	Т	K	30
2	229	G	L	T	R	E	A	o Q	A	K	27
3	145	К	I	Ġ	V	A	A	V	V	R	26
4	150	A	v	v V	R	G	A	Ă	L	м	24
5	290	P	I	v	Y	G	V	K	Т	K	24
6	35	s	L	Y	L	I	Ā	V	L	G	23
7	156	A	L	± M	A	P	L	P	v	F	23
8	47	I	I	Y	I	V	≓ R	T	Ē	н	22
9	50	I	v	R	Т	E	H	s	L	н	22
10	142	Ŕ	v	T	K	I	G	v	A	A	22
11	151	v	v	÷ R	G	A	≚ A	Ļ	М	A	22
12	242	C	v	S	Н	v	C	= A	v	F	22
13	248	A	v	F	I	F	Y	v	P	F	22
14	116	v	L	- L	Ā	M	Ã	F	D	R	21
15	192	D	D	I	R	v	N	v	v	Y	21
16	303	R	I	L	R	L	F	H	v	A	21
17	304	I	L	= R	L	F	H	v	A	T	21
18	108	s	L	s	G	М	E	s	Т	v	20
19	198	v	v	Y	G	L	I	v	Ī	I	20
20	291	I	v	Y	G	v	K	T	K	E	20
21	15	I	L	Ī	G	L	P	G	L	E	19
22	44	N	L	T	I	I	Y	I	V	R	19
23	73	I	L	Ī	s	т	S	S	М	P	19
24	74	L	I	S	Т	s	S	M	P	ĸ	19
25	99	С	L	L	Q	Ι	F	A	Ι	н	19
26	162	P	v	F	Ι	K	Q	L	P	F	19
27	203	1	v	I	1	s	A	I	G	L	19
28	221	L	L	Ī	L	K	Т	v	L	G	19
29	245	Н	v	C	Α	V	F	I	F	Y	19
30	306	R	L	F	Н	V	A	T	Н	A	19
31	40	A	v	L	G	N	L	T	Ι	I	18
32	85	Α	I	F	W	F	N	s	Т	T	18
33	205	I	I	s	Α	Ι	G	Ŀ	D	S	18
34	220	Y	L	L	I	L	K	T	V	L	18
35	253	Y	v	P	F	I	G	L	S	M	18
36	37	Y	L	I	Α	V	$\underline{\mathbf{L}}$	G	N	L	17
37	41	V	L	G	N	L	T	Ī	Ι	Y	17
38	117	L	L	A	М	Α	F	D	R	Y	17
39	131	P	L	R	Н	Α	$\underline{\mathbf{T}}$	\underline{v}	L	T	17
40	136	T	v	F	T	L	P	$\underline{\mathbf{R}}$	V	T	17
											19

HLA-A3 nonomers(SEQ ID NOS 1676-1747, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
41	180	Y	C	L	Н	Q	D	v	М	ĸ	17
42	201	G	L	= I	v	I	I	s	Α	I	17
43	213	s	L	L	Ι	s	F	s	Y	L	17
44	256	F	I	G	L	s	M	v	Н	R	17
45	261	М	v	H	R	F	s	K	R	R	17
46	276	I	L	A	N	I	Y	L	L	v	17
47	281	Y	L	L	٧	P	P	v	L	N	17
48	286	P	v	L	N	P	Ī	V	Y	G	17
49	288	L	N	P	Ι	V	Y	G	V	ĸ	17
50	309	Н	v	A	T	Н	A	ś	Ε	P	17
51	1	M	v	$\underline{\mathtt{D}}$	P	N	G	N	Е	s	16
52	56	S	L	H	E	P	$\underline{\underline{M}}$	$\underline{\underline{Y}}$	1	F	16
53	70	G	Ι	$\underline{\mathtt{D}}$	Ι	\mathbf{L}	$\overline{\mathbf{I}}$	\underline{s}	T	S	16
54	72	D	I	$\underline{\mathbf{L}}$	Ι	S	$\underline{\underline{\mathbf{T}}}$	$\underline{\underline{s}}$	s	M	16
55	115	\mathbf{T}	v	$\underline{\mathbf{r}}$	L	A	$\underline{\underline{M}}$	<u>A</u>	F	D	16
56	125	Y	V	$\underline{\underline{A}}$	Ι	С	$\overline{\mathbf{H}}$	<u>P</u>	L	R	16
57	144	Т	K	Ī	G	V	$\underline{\underline{A}}$	<u>A</u>	V	v	16
58	167	Q	L	$\underline{\mathbf{P}}$	F	С	$\underline{\mathbf{R}}$	$\underline{\mathbf{S}}$	N	I	16
59	175	I	L	<u>s</u>	Η	S	$\underline{\mathtt{Y}}$	$\underline{\mathtt{C}}$	L	Н	16
60	195	R	v	\overline{N}	V	V	$\underline{\underline{Y}}$	$\underline{\mathbf{G}}$	L	I	16
61	197	N	v	V	Y	G	$\overline{\mathbf{r}}$	Ī	V	I	16
62	210	G	L	$\overline{\mathbf{D}}$	S	L	$\overline{\Gamma}$	$\underline{\mathtt{I}}$	S	F	16
63	282	L	L	$\overline{\Lambda}$	P	P	Ā	$\overline{\Gamma}$	N	P	16
64	299	E	I	R	Q	R	Ī	Ē	R	L	16
65	301	R	Q	\underline{R}	Ι	L	\underline{R}	$\overline{\Gamma}$	F	Н	16
66	16	\mathbf{L}	Ι	\underline{G}	L	Þ	\underline{G}	$\overline{\Gamma}$	Е	E	15
67	46	Т	I	Ī	Y	Ι	$\overline{\Lambda}$	$\underline{\underline{R}}$	Т	Ε	15
68	102	Q	I	$\frac{\mathbf{F}}{}$	A	Ι	<u>H</u>	<u>s</u>	L	s	15
69	193	D	Ι	<u>R</u>	V	N	$\overline{\Lambda}$	$\overline{\Lambda}$	Y	G	15
70	208	A	I	$\underline{\mathbf{G}}$	L	D	$\underline{\mathbf{s}}$	$\underline{\underline{\mathbf{L}}}$	L	I	15
71	223	Ι	L	<u>K</u>	T	V	F	G	L	T	15
72	237	K	A	F	G	T	\underline{c}	$\overline{\Lambda}$	S	H	15

HLA-B*0702 nonomers(SEQ ID NOS 1748-1812, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	130	Н	P	L	R	Н	Α	Т	V	L	22
2	59	E	P	М	Y	I	F	L	С	M	21
3	168	\mathbf{L}	P	F	C	R	s	N	I	L	20
4	289	N	P	I	V	Y	G	V	K	T	19
5	3	D	P	N	G	N	E	S	S	A	18
6	19	L	P	G	L	E	E	Α	Q	F	18
7	140	\mathbf{L}	P	R	V	T	K	Ι	G	v	18
8	284	V	P	P	V	L	N	Р	I	v	17
9	31	F	P	L	C	s	L	Y	L	I	16
10	254	V	P	F	I	G	L	Ş	М	v	16
11	269	R	D	S	P	L	Ρ	V	Ι	L	16
											20

HLA-B*0702 nonomers(SEQ ID NOS 1748-1812, respectively in order of appearance)

				-	-						
	Pos	1	2	3	4	5	6	7	8	9	score
12	149	A	A	V	V	R	G	A	A	L	15
13	153	R	G	A	A	L	М	A	P	L	15
14	156	A	L	М	A	P	L	P	V	F	15
15		I			V						
	251		F	Y		P	F	I	G	L	15
16	299	E	I	R	Q	R	I	Ļ	R	L	15
17	8	E	S	S	A	Т	Y	F	Ι	L	14
18	28	W	ь	A	F	P	L	C	S	L	14
19	30	A	F	P	L	C	S	Ь	Y	L	14
20	110	S	G	M	E	S	Т	V	Ь	L	14
21	132	L	R	Н	A	Т	V	L	Т	L	1.4
22	159	A	P	L	P	V	F	Ι	K	Q	14
23	222	L	Ι	Г	K	Т	V	L	G	L	14
24	271	S	P	L	P	V	Ι	L	A	N	14
25	25	A	Q	F	W	L	Α	F	Р	L	13
26	109	L	S	G	M	E	S	Т	V	L	13
27	124	R	Y	V	A	Ι	C	Н	Р	L	13
28	216	Ι	S	F	S	Y	L	L	Ι	L	13
29	268	R	R	D	S	P	L	Þ	V	I	13
30	280	I	Y	L	L	V	Ρ	Р	V	L	13
31	11	A	T	Y	F	Ι	L	Ι	G	L	12
32	34	С	S	L	Y	L	Ι	A	V	L	12
33	57	L	H	Е	P	M	Y	I	F	L	12
34	76	S	T	S	S	M	P	K	М	L	12
35	142	R	v	T	K	1	G	V	A	A	12
36	151	V	V	R	G	Α	A	L	М	A	12
37	190	А	С	D	D	I	R	V	N	v	12
38	194	I	R	V	N	V	V	Y	G	L	12
39	206	I	S	A	Ι	G	L	D	S	L	12
40	207	S	A	Ι	G	L	D	S	L	L	12
41	220	Y	L	\mathbf{L}	Ι	L	K	T	V	L	12
42	267	K	R	R	D	S	P	L	P	V	12
43	304	I	L	R	L	F	H	V	Α	T	12
44	14	F	I	L	Ι	G	L	P	G	L	11
45	23	E	E	Α	Q	F	W	L	Α	F	11
46	37	Y	L	I	A	V	L	G	N	L	11
47	40	Α	V	L	G	N	L	Т	I	I	11
48	77	Т	s	S	M	P	K	М	L	A	11
49	78	S	s	М	P	K	М	L	Α	I	11
50	80	М	P	K	M	\mathbf{L}	Α	I	F	W	11
51	92	T	T	I	Q	F	D	А	C	L	11
52	112	M	E	s	\mathbf{T}	V	L	L	Α	M	11
53	119	Α	M	Α	F	D	R	Y	V	A	11
54	127	Α	I	С	Н	P	L	R	Н	A	11
55	131	P	L	R	Н	Α	Т	v	L	T	11
56	155	Α	A	L	М	Α	P	L	P	v	11
57	157	L	M	Α	P	L	P	v	F	I	11
58	181	С	L	Н	Q	D	v	M	K	L	11
59	203	I	v	I	I	S	Α	Ι	G	L	11
60	208	Α	I	G	L	D	s	L	L	I	11
											21

HLA-B*0702 nonomers(SEQ ID NOS 1748-1812, respectively in order of appearance)

	Pos										score
	105	1	2	3	4	5	6	7	8	9	SCOLE
61	213	S	L	L	I	S	F	S	Y	L	11
62	248	Α	v	F	I	F	Y	V	P	F	11
63	265	F	s	K	R	R	D	s	P	L	11
64	275	V	I	L	Α	N	I	Y	L	L	11
65	285	Р	P	v	L	N	р	Τ	v	Y	1.1

HLA-B*08 nonomers(SEQ ID NOS 1813-1847, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	R	Ô	R	I	Ĺ	R	Ĺ	31
2	265	F	s	ĸ	R	R	D	s	P	L	29
3	149	A	A	v	v	R	G	A	A	L	24
4	168	L	P	F	C	R	s	N	I	L	24
5	294	G	V	ĸ	Т	ĸ	E	I	R	Q	21
6	120	М	Α	F	D	R	Y	V	Α	ī	20
7	292	v	Y	G	v	ĸ	Т	K	Е	Ι	20
8	21	G	L	E	Ε	Α	Q	F	W	L	19
9	78	s	S	М	P	ĸ	М	L	Α	I	19
10	160	P	L	P	V	F	Ι	K	Q	L	19
11	186	V	М	ĸ	L	A	С	D	D	I	18
12	213	S	L	L	I	s	F	S	Y	L	18
13	221	L	L	I	L	ĸ	\mathbf{T}	V	L	G	18
14	296	K	Т	ĸ	E	I	R	Q	R	I	18
15	297	\mathbf{T}	K	E	Ι	R	Q	R	I	L	18
16	130	H	P	L	R	Н	Α	T	V	L	17
17	181	С	L	Н	Q	D	V	М	K	L	17
18	223	I	L	K	Т	v	\mathbf{L}	G	L	T	17
19	28	W	L	A	F	P	L	C	S	L	16
20	37	Y	L	I	A	v	L	G	N	L	16
21	56	S	L	H	Е	P	М	Y	I	F	16
22	80	М	P	K	М	L	Α	1	F	W	16
23	162	P	V	F	Ι	K	Q	L	P	F	16
24	201	G	L	I	V	I	Ι	S	A	I	16
25	207	S	Α	Ι	G	L	D	S	L	L	16
26	214	L	L	I	S	F	S	Y	L	L	16
27	220	Y	L	L	Ι	L	K	Т	V	L	16
28	233	E	A	Q	A	K	A	F	G	T	16
29	275	V	Ι	L	A	N	Ι	Y	L	L	16
30	304	Ι	L	R	L	F	Н	V	A	T	16
31	14	F	Ι	L	Ι	G	L	Ρ	G	L	15
32	110	S	G	M	Ε	S	Т	V	L	L	15
33	138	L	T	L	P	R	V	Т	K	I	15
34	164	F	Ι	K	Q	L	P	F	С	R	15
35	222	L	Ι	L	K	T	V	L	G	L	15

HLA-B*1510 nonomers(SEQ ID NOS 1848-1890, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	57	L	Н	E	P	М	Y	ï	F	L	23
2	244	s	н	V	C	A	V	F	I	F	17
3	269	R	D	s	P	L	P	V	I	L	16
4	280	I	Y	L	L	V	P	P	V	L	16
5	262	V	н	R	F	s	K	R	R	D	15
6	299	Ē	I	R	0	R	I	L	R	L	15
7	106	ī	н	S	L	S	G	М	E	S	14
8	206	I	s	A	I	G	L	D	S	L	14
9	220	Y	L	L	ı	L	К	Т	V	L	14
10	251	I	F	Y	v	P	F	I	G	L	14
11	297	Т	ĸ	E	I	R	Q	R	I	L	14
12	21	G	L	E	E	A	Q	F	W	L	13
13	34	C	s	L	Y	L	ĭ	Ā	v	L	13
14	54	E	н	S	L	Н	E	P	M	Y	13
15	110	s	G	М	E	s	Т	v	L	L	13
16	194	I	R	v	N	v	v	Y	G	L	13
17	8	E	S	s	A	Т	Y	F	I	L	12
18	14	F	I	L	Ι	G	L	P	G	L	12
19	28	W	L	Α	F	P	L	C	s	L	12
20	66	С	М	L	s	G	I	D	I	L	12
21	76	s	Т	S	s	М	Р	K	М	L	12
22	92	Т	T	Ι	Q	F	D	Α	C	L	12
23	109	L	s	G	M	E	s	Т	v	L	12
24	130	Н	P	L	R	Н	Α	Т	v	L	12
25	132	\mathbf{L}	R	Н	Α	Т	V	L	Т	L	12
26	149	Α	A	V	V	R	G	A	Α	L	12
27	153	R	G	A	Α	L	М	Α	P	L	12
28	160	P	L	P	V	F	I	K	Q	L	12
29	181	C	L	Н	Q	D	V	М	K	L	12
30	182	L	Н	Q	D	V	M	K	L	A	12
31	203	I	v	I	Ι	S	Α	I	G	L	12
32	216	I	S	F	S	Y	L	L	I	L	12
33	222	L	I	L	K	T	V	L	G	L	12
34	275	V	I	L	A	N	Ι	Y	L	L	12
35	37	Y	L	I	Α	V	L	G	N	L	11
36	49	Y	Ι	٧	R	Т	Е	Н	S	L	11
37	93	\mathbf{T}	I	Q	F	D	A	C	L	L	11
38	101	L	Q	Ι	F	Α	Ι	Н	S	L	11
39	129	C	H	P	L	R	Н	Α	Т	v	11
40	133	R	H	A	Т	V	L	Т	L	P	11
41	177	S	H	S	Y	С	L	Н	Q	D	11
42	207	S	A	I	G	L	D	S	L	L	11
43	257	I	G	L	S	М	V	Н	R	F	11

HLA-B*2705 nonomers (SEQ ID NOS 1891-2008, respectively in order of appearance)

HLA-B*2705 nonomers(SEQ ID NOS 1891-2008, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	194	I	R	V	N	V	V	Y	G	L	25
2	268	R	R	D	s	P	L	P	V	I	24
3	132	L	R	Н	A	T	v	L	Т	L	23
4	300	I	R	Q	R	I	L	R	L	F	23
5	305	L	R	L	F	H	v	A	Т	Н	23
6	231	Т	R	Ė	A	Q	Ā	К	Ā	F	21
7	34	C	S	L	Y	L	I	A	V	L	18
8	299	E	I	R	Q	R	I	L	R	L	18
9	6	G	N	Е	s	S	A	Т	Y	F	17
10	66	С	м	L	s	G	Ι	D	I	L	17
11	162	P	v	F	Ι	K	Q	L	P	F	17
12	207	S	Α	1	G	L	D	s	L	L	17
13	210	G	L	D	S	L	L	I	s	F	17
14	220	Y	L	L	I	L	K	Т	V	L	17
15	237	K	Α	F	G	Т	С	v	s	н	17
16	269	R	D	s	Р	L	P	v	I	L	17
17	280	I	Y	L	L	v	P	Р	v	L	17
18	295	v	ĸ	т	K	Ε	I	R	Q	R	17
19	11	Α	т	Y	F	I	L	Ι	G	L	16
20	14	F	I	L	I	G	L	Р	G	L	16
21	21	G	L	E	E	Α	Q	F	W	L	16
22	25	Α	Q	F	W	L	Α	F	P	L	16
23	37	Y	L	1	A	v	L	G	N	L	16
24	92	T	т	Ι	Q	F	D	Α	С	L	16
25	101	L	Q	I	F	Α	Ι	Н	s	L	16
26	124	R	Y	V	Α	I	С	Н	P	L	16
27	130	H	P	L	R	Н	Α	Т	V	L	16
28	141	P	R	V	T	K	Ι	G	V	A	16
29	153	R	G	А	Α	L	М	Α	P	L	16
30	181	С	L	Н	Q	D	V	М	K	L	16
31	201	G	L	I	V	Ι	Ι	S	A	I	16
32	203	I	V	1	Ι	S	Α	Ι	G	L	16
33	216	I	S	F	S	Y	L	\mathbf{L}	I	L	16
34	222	L	I	L	K	Т	V	L	G	L	16
35	255	P	F	Ι	G	L	S	M	V	H	16
36	257	I	G	L	S	M	V	Η	R	F	16
37	275	V	Ι	L	A	N	Ι	Y	L	L	16
38	47	I	Ι	Y	Ι	V	R	Т	E	н	15
39	109	L	S	G	M	E	S	Т	V	L	15
40	114	S	Т	V	L	L	A	M	A	F	15
41	123	D	R	Y	V	A	Ι	C	Н	P	15
42	145	K	Ι	G	V	A	Ą	V	V	R	15
43	156	A	L	M	A	P -	L	Р	V	F	15
44	168	L	P	F	C	R	s	N	Ι	L	15
45	172	R	s	N	I	L	S	Н	s	Y	15
46	198	V	v	Y	G	L	1	V	I	I	15
47	206	I	s	A	I	G	L	D	S	L	15
48	229	G	L	Т	R	E	A	Q	A	K	15
49	248	A	V	F	Ι	F	Y	V	P	F	15 24

HLA-B*2705 nonomers(SEQ ID NOS 1891-2008, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
50	251	I	F	Y	V	Р	F	ı	G	L	15
51	274	P	v	I	L	A	N	I	Y	L	15
52	290	P	I	V	Y	G	V	K	Т	K	15
53	298	K	E	I	R	0	R	I	L	R	15
54	19	L	P	G	L	E	E	A	0	F	14
55	29	L	A	F	Ь	L	C	S	L	Y	14
56	30	A	F	Р	L	С	s	L			14
57	39	I	A	V	L	G	N	ь	Y T	L	
58		A	v	v L			L				14
59	40	S	M	Р	G K	N	L	T	I	I	14 14
60	79		K	М	L	M	ı	A F	I	F	14 14
	81	P				A			W	F	
61	99	C	L	L	Q	I	F	A	I	H	14
62	137	V	L	T	L	P	R	V	T	K	14
63	138	L	T	L	P	R	V	T	K	I	14
64	150	A	v -	V	R	G	A	A	L	M	14
65	160	P	L	P	V	F	I	K	Q	L	14
66	174	N	I	L	S	H	S	Y	C	L	14
67	180	Y -	C	L	H	Q	D	V	M	K	14
68	192	D	D	Ι	R	V	N	V	V	Y	14
69	212	D	S	L	L	Ι	S	F	S	Y	14
70	213	S	L	L	Ι	S	F	S	Y	L	14
71	214	L	L	Ι	S	F	S	Y	L	L	14
72	260	S	M	V	Н	R	F	S	K	R	14
73	263	H	R	F	S	K	R	R	D	S	14
74	267	K	R	R	D	S	P	L	P	V	14
75	293	Y	G	V	K	T	K	Ε	Ι	R	14
76	301	R	Q	R	I	L	R	L	F	Н	14
77	302	Q	R	I	L	R	L	F	Η	V	14
78	5	N	G	N	Ε	S	S	A	Т	Y	13
79	23	E	Е	A	Q	F	W	L	A	F	13
80	28	W	L	A	F	Р	L	С	S	L	13
81	44	N	L	Т	Ι	Ι	Y	Ι	V	R	13
82	51	V	R	Т	E	Н	S	L	H	Е	13
83	56	S	L	Н	E	P	M	Y	Ι	F	13
84	60	P	M	Y	Ι	F	L	С	M	L	13
85	72	D	Ι	L	Ι	S	T	S	S	M	13
86	74	L	I	S	Т	S	S	M	Р	K	13
87	75	I	S	T	S	S	M	P	K	M	13
88	98	A	C	L	\mathbf{L}	Q	Ι	F	A	I	13
89	104	F	A	Ι	Н	S	L	S	G	M	13
90	110	S	G	M	E	S	Т	V	L	L	13
91	116	V	L	L	Α	М	Α	F	D	R	13
92	126	V	A	Ι	C	Н	P	L	R	H	13
93	149	A	A	٧	V	R	G	Α	Α	L	13
94	158	M	A	P	L	P	V	F	I	K	13
95	164	F	I	K	Q	L	P	F	С	R	13
96	170	F	C	R	s	N	I	L	S	H	13
97	171	С	R	S	N	I	L	S	Н	s	13
98	187	М	K	L	Α	C	D	D	1	R	13
											25

HLA-B*2705 nonomers(SEQ ID NOS 1891-2008, respectively in order of appearance)

	Pos										score
		1	2	3	4	5	6	7	8	9	
99	217	S	F	S	Y	\mathbf{L}	\mathbf{L}	1	L	K	13
100	224	L	K	\mathbf{T}	V	L	G	L	T	R	13
101	242	C	v	S	Н	V	С	Α	V	F	13
102	256	F	I	G	L	S	Μ	V	Н	R	13
103	261	M	v	Н	R	F	S	K	R	R	13
104	49	Y	I	V	R	Т	Е	Н	S	L	12
105	57	L	H	E	P	M	Y	Ι	F	L	12
106	88	W	F	N	S	T	\mathbf{T}	I	Q	F	12
107	96	F	D	Α	C	L	L	Q	1	F	12
108	134	Н	A	\mathbf{T}	V	L	\mathbf{T}	L	P	R	12
109	152	V	R	G	Α	Α	L	М	Α	P	12
110	179	s	Y	C	L	Н	Q	D	V	M	12
111	197	N	v	V	Y	G	L	Ι	V	I	12
112	244	S	H	V	C	A	V	F	I	F	12
113	265	F	S	K	R	R	D	S	P	L	12
114	273	L	P	V	I	L	Α	N	I	Y	12
115	285	P	P	V	L	N	P	Ι	V	Y	12
116	288	L	N	P	Ι	V	Y	G	V	ĸ	12
117	296	K	T	K	E	1	R	Q	R	I	12
118	297	T	ĸ	E	1	R	Q	R	I	L	12

HLA-B*2709 nonomers(SEQ ID NOS 2009-2063, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	194	I	R	v	N	v	v	Y	G	L	24
2	268	R	R	D	s	Р	L	Р	v	I	24
3	132	\mathbf{L}	R	Н	A	Т	V	L	Т	L	22
4	267	K	R	R	D	s	P	L	Р	V	21
5	300	I	R	Q	R	Ι	L	R	L	F	20
6	231	\mathbf{T}	R	E	Α	Q	A	K	Α	F	19
7	302	Q	R	I	L	R	L	F	Н	V	19
8	124	R	Y	V	Α	I	С	Н	P	L	16
9	269	R	D	S	P	L	P	V	I	L	16
10	43	G	N	L	T	Ι	Ι	Y	Ι	V	15
11	216	I	S	F	S	Y	L	L	Ι	L	15
12	11	A	\mathbf{T}	Y	F	Ι	L	Ι	G	L	14
13	25	Α	Q	F	W	L	A	F	P	L	14
14	153	R	G	A	A	L	М	Α	P	L	14
15	174	N	I	L	S	Н	s	Y	C	L	14
16	222	L	I	L	K	T	V	L	G	L	14
17	257	I	G	L	S	M	V	Н	R	F	14
18	280	I	Y	L	L	V	₽	P	V	L	14
19	6	G	N	E	S	S	Α	T	Y	F	13
20	14	F	I	L	Ι	G	L	P	G	L	13
21	21	G	L	Е	E	A	Q	F	W	L	13
22	66	С	M	L	S	G	I	D	I	L	13
	•										26

HLA-B*2709 nonomers(SEQ ID NOS 2009-2063, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
23	130	Н	Ρ	L	R	Н	Α	Т	V	L	13
24	201	G	L	Ι	v	Ι	I	s	Α	I	13
25	203	I	V	Ι	Ι	S	Α	Ι	G	L	13
26	214	L	L	Ι	s	F	S	Y	L	L	13
27	251	I	F	Y	V	P	F	I	G	L	13
28	263	Н	R	F	S	K	R	R	D	S	13
29	275	V	Ι	L	Α	N	I	Y	L	L	13
30	305	L	R	L	F	Н	V	Α	Т	Н	13
31	30	Α	F	P	L	C	S	L	Y	L	12
32	34	C	S	L	Y	L	I	Α	V	L	12
33	37	Y	L	Ι	Α	V	L	G	N	L	12
34	51	V	R	T	E	Н	S	\mathbf{L}	Н	Е	12
35	60	P	М	Y	Ι	F	L	С	M	L	12
36	75	I	S	Т	S	S	М	P	K	М	12
37	93	T	I	Q	F	D	Α	С	L	L	12
38	123	D	R	Y	V	Α	I	C	Н	P	12
39	135	A	Т	V	L	T	L	Ρ	R	V	12
40	138	L	Т	L	P	R	V	T	K	I	12
41	149	Α	A	V	V	R	G	Α	Α	L	12
42	155	Α	A	L	M	A	Ρ	L	P	V	12
43	168	L	P	F	C	R	S	N	Ι	L	12
44	181	C	L	Н	Q	D	V	M	K	L	12
45	188	K	L	A	C	D	D	I	R	V	12
46	190	Α	С	D	D	Ι	R	V	N	V	12
47	195	R	V	N	V	V	Y	G	\mathbf{L}	I	12
48	210	G	L	D	S	L	L	Ι	S	F	12
49	213	S	L	L	Ι	S	F	S	Y	L	12
50	220	Y	L	L	Ι	L	K	T	V	L	12
51	248	A	V	F	Ι	F	Y	V	P	F	12
52	279	N	Ι	Y	L	L	V	P	P	V	12
53	287	V	L	N	Ρ	Ι	V	Y	G	V	12
54	296	K	T	K	E	I	R	Q	R	I	12
55	299	E	Ι	R	Q	R	I	\mathbf{r}	R	\mathbf{L}	12

HLA-B*5101 nonomers(SEQ ID NOS 2064-2132, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	39	I	A	V	L	G	N	L	Т	I	26
· 2	31	F	P	L	C	S	Ļ	Y	L	I	25
3	120	М	A	F	D	R	Y	V	Α	I	24
4	130	H	P	L	R	Н	A	Т	V	L	23
5	118	L	A	М	A	F	D	R	Y	v	22
6	140	L	P	R	V	\mathbf{T}	K	Ι	G	v	22
7	155	A	A	L	М	Α	P	L	P	v	22
8	42	L	G	N	L	Т	Ι	Ι	Y	I	21
9	254	V	P	F	I	G	L	S	M	v	21
10	284	V	P	P	V	L	N	P	Ι	v	21
											27

HLA-B*5101 nonomers (SEQ ID NOS 2064-2132, respectively in order of appearance)

	Pos	-	_	2		ŗ.	_	-7	0		score
	1.00	1	2	3	4	5	6	7	8	9	2.2
11	168	L	P	F	C	R	s	N	I	L	20
12	235	Q	A -	K	A	F	G	Т	C	v -	20
13	138	L	T	L	P	R	V	Т	K	I	19
14	159	A	P	L	P	V	F	Ι	K	Q	18
15	189	L	A	С	D	D	Ι	R	V	N	18
16	198	V	v	Y	G	L	Ι	V	Ι	Ι	18
17	277	L	A	N	Ι	Y	L	L	V	P	18
18	207	S	Α	I	G	L	D	S	L	L	17
19	283	L	V	P	P	V	L	N	P	I	17
20	63	I	F	L	С	M	L	S	G	I	16
21	86	I	F	W	F	N	S	Т	Т	Ι	16
22	110	S	G	M	Ε	S	T	V	L	L	16
23	144	Т	K	Ι	G	V	A	A	V	V	16
24	149	A	A	V	V	R	G	A	A	L	16
25	197	N	V	V	Y	G	L	Ι	V	I	16
26	271	S	P	L	P	V	Ι	L	A	N	16
27	280	I	Y	L	L	V	P	Р	V	L	16
28	3	D	P	N	G	N	E	S	S	A	15
29	40	Α	V	L	G	N	L	Т	Ι	I	15
30	97	D	A	С	L	L	Q	1	F	A	15
31	132	L	R	Н	А	T	V	L	T	L	15
32	222	L	I	L	K	Т	V	L	G	L	15
33	279	N	I	Y	L	L	V	P	P	\mathbf{v}	15
34	285	Þ	P	V	L	N	P	I	V	Y	15
35	289	N	P	I	V	Y	G	V	K	T	15
36	9	S	S	А	Т	Y	F	I	L	I	14
37	65	\mathbf{L}	C	M	L	S	G	1	D	I	14
38	84	L	A	Ι	F	W	F	N	S	T	14
39	126	V	A	Ι	С	Н	P	L	R	Н	14
40	157	L	M	Α	P	L	P	V	F	I	14
41	158	M	A	P	L	P	V	F	Ι	K	14
42	191	C	D	D	Ι	R	V	N	V	V	14
43	200	Y	G	L	I	V	Ι	Ι	S	A	14
44	209	I	G	L	D	S	L	L	I	S	14
45	215	L	I	S	F	S	Y	L	L	I	14
46	219	S	Y	L	L	Ι	L	K	T	٧	14
47	220	Y	L	L	Ι	L	K	\mathbf{T}	V	L	14
48	237	K	A	F	G	Т	С	V	S	Н	14
49	247	С	A	V	F	I	F	Y	V	P	14
50	249	V	F	1	F	Y	V	Р	F	I	14
51	251	Ι	F	Y	V	P	F	1	G	L	14
52	257	I	G	L	S	M	V	H	R	F	14
53	268	R	R	D	S	P	L	Р	V	I	14
54	273	L	P	V	Ι	L	Α	N	I	Y	14
55	29	L	A	F	P	L	С	s	L	Y	13
56	33	L	C	S	L	Y	L	I	A	v	13
57	55	Н	s	L	Н	E	P	M	Y	I	13
58	67	M	L	s	G	I	D	Ι	L	I	13
59	80	М	P	K	M	L	Α	I	F	W	13
											28

HLA-B*5101 nonomers(SEQ ID NOS 2064-2132, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
60	95	Q	F	D	Ā	C	L	L	Q	I	13
61	98	Α	С	L	L	Q	Ι	F	Α	I	13
62	104	F	A	Ι	Н	s	L	s	G	M	13
63	146	I	G	V	Α	Α	V	V	R	G	13
64	148	V	Α	A	V	V	R	G	Α	A	13
65	153	R	G	A	Α	L	М	Α	P	L	13
66	233	E	A	Q	A	K	Α	F	G	T	13
67	243	V	S	Н	V	C	Α	V	F	I	13
68	292	V	Y	G	V	K	Т	K	Е	I	13
69	296	K	T	K	E	I	R	Q	R	I	13

Please replace Table XXVII, beginning at page 201, line 1, with the following rewritten

Table XXVII:

--Table XXVII:

HLA Class I decamers

HLA-A1 decamers (SEQ ID NOS 2133-2153, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	191	C	$\underline{\mathtt{D}}$	D	1	R	V	N	V	v	Y	27
2	244	s	H	v	C	A	V	F	I	F	Y	24
3	40	Α	\underline{v}									21
4	284	V	$\underline{\mathbf{P}}$	P	V	L	N	P	1	v	Y	21
5	116	V	ഥ	L	A	М	Α	F	D	R	Y	20
6	28	W	Ŀ	A	F	P	L	\underline{c}	S	L	Y	18
7	297	т	K	E	Ι	R	Q	R	I	L	R	17
8	21	G	Ŀ	E	E	A	Q	F	W	L	Α	16
9	22	L	E	E	A	Q	F	\underline{W}	L	A	F	16
10	52	R	$\underline{\mathbf{T}}$	E	Н	S	L	$\underline{\mathbf{H}}$	E	P	М	16
11	53	T	E	H	S	\mathbf{L}	Н	E	P	M	Y	16
12	57	L	$\underline{\mathbf{H}}$	E	P	М	Y	I	F	L	C	16
13	111	G	M	E	S	T	V	$\underline{\underline{\mathbf{r}}}$	L	A	М	16
14	272	P	$\overline{\mathbf{L}}$	P	V	Ι	L	$\underline{\underline{A}}$	N	I	Y	16
15	1	M	\underline{v}	D	P	N	G	$\overline{\mathbf{N}}$	E	S	S	15
16	4	P	N	G	N	E	s	\underline{s}	Α	T	Y	15
17	121	A	F	D	R	Y	V	A	Ι	C	Н	15
18	171	C	R	S	N	Ι	L	$\underline{\underline{s}}$	Н	s	Y	15
19	211	L	$\overline{\mathbf{D}}$	S	L	L	Ι	S	F	S	Y	15
20	8	E	<u>s</u>	s	Α	Т	Y	F	1	L	Ι	13
21	190	Α	\underline{C}	D	D	I	R	\underline{v}	N	V	V	13

HLA-A*0201 decamers(SEQ ID NOS 2154-2253, respectively in order of appearance)

Pos 1 2 3 4 5 6 7 8 9 0 score

HLA-A*0201 decamers (SEQ ID NOS 2154-2253, respectively in order of appearance)

	ın ora		a	рp	ea	ra	nc	e)			
	Pos	1 2	3	4	5	6	7	8	9	0	score
1	221	L L	Ι	L	K	$\underline{\mathbf{T}}$	V	L	G	L	30
2	100	L L	Q	Ι	F	$\underline{\mathbf{A}}$	Ι	Н	S	L	29
3	282	L L	V	P	P	\underline{v}	L	N	P	Ι	27
4	205	ΙI	S	Α	Ι	$\underline{\mathbf{G}}$	L	D	s	L	26
5	213	SL	L	1	s	F	s	Y	L	L	25
6	56	S L	Н	E	Р	М	Y	Ι	F	L	24
7	62	Y I	F	L	С	М	L	S	G	Ι	24
8	108	SL	S	G	М	E	s	\mathbf{T}	v	L	24
9	117	L L	Α	М	Α	F	D	R	Y	V	24
10	131	РL	R	H	Α	$_{ m T}$	V	L	T	L	24
11	137	V L	Т	ь	P	R	V	Т	ĸ	Ι	24
12	215	L I	s	F	s	Y	L	L	I	Ь	24
13	38	LI	Α	v	L	G	N	L	т	Ι	23
14	41	VL	G	N	L	T	Ι	Ι	Y	Ι	23
15	156	A L	М	Α	Р	L	P	V	F	Ι	23
16	193	D I	R	V	N	v	V	Y	G	L	23
17	214	L L	Ι	s	F	s	Y	L	L	I	23
18	32	Р L	С	s	L	Ÿ	L	Ι	Α	v	22
19	119	A M	Α	F	D	R	Y	V	Α	Ι	22
20		КА	F	G	Т	C	v	S	н	v	22
21	275	VI	L	A	N	Ī	Y	L	L	v	22
22	85	ΑI	F	W	F	N	s	Т	Т	Ι	21
23	139	T L	Р	R	v	T	K	I	G	v	21
24	202	LТ	v	Ι	Ι	s	Α	Ι	G	L	21
25	13	Y F	I	L	Ι	G	L	P	G	L	20
26	16	LI	G	L	Р	G	L	Е	E	Α	20
27	29	LA	F	P	L	C	s	L	Y	L	20
28	142	R V	Т	K	Ι	G	v	Α	A	v	20
29	148	V A	Α	v	V	R	G	Α	A	L	20
30	167	QL	P	F	С	R	S	N	I	L	20
31	180	Y C	L	Н	Q	D	V	М	ĸ	L	20
32	222	LI	L	K	Т	v	L	G	L	Т	20
33	240	G T	С	v	S	H	V	С	A	v	20
34	248	A V	F	I	F	Y	V	P	F	Ι	20
35	250	FI	F	Y	V	P	F	Ι	G	L	20
36	271	SP	L	P	V	I	L	Α	N	Ι	20
37	279	N I	Y	L	L	V	P	P	v	L	20
38	304	I L	R	L	F	H	V	Α	T	Н	20
39	10	SA	Т	Y	F	I	L	Ι	G	L	19
40	15	I L	Ι	G	L	P	G	L	E	Е	19
41	27	F W	L	A	F	P	L	С	s	L	19
42	35	S L	Y	L	Ι	A	V	L	G	N	19
43	37	Y L	I	Α	V	L	G	N	L	Т	19
44	44	N L	Т	Ι	I	Y	Ι	V	R	Т	19
45	64	F L	С	М	L	S	G	I	D	Ι	19
46	83	M L	Α	Ι	F	W	F	N	s	Т	19
47	159	A P	L	P	V	F	I	K	Q	L	19
48	189	L A	С	D	D	I	R	V	N	v	19
49	207	SA	I	G	L	D	s	L	L	Ι	19
50	253	Y V	Р	F	I	G	L	S	M	V	19
											30

HLA-A*0201 decamers(SEQ ID NOS 2154-2253, respectively in order of appearance)

		uc_	~ -	u	PP	ψu	- 4		٠,			
	Pos	1	2	3	4	5	6	7	8	9	0	score
51	276	I	L	Α	N	Ι	Y	L	L	v	Р	19
52	281	Y	L	L	v	Р	P	V	L	N	Р	19
53	283	L	v	Р	Р	V	L	N	Р	I	V	19
54	286	P	v	L	N	Р	I	V	Y	G	V	19
55	33	L	C	s	L	Y	L	Ι	A	v	L	18
56	36	L	Y	L	I	A	v	L	G	N	L	18
57	39	I	A	v	L	G	Ň	L	Т	I	I	18
58	42	_ L	G	N	L	Т	I	I	Y	I	v	18
59	66	C	М	L	s	G	Ī	D	ī	L	I	18
60	111	G	M	E	s	Т	v	L	L	A	M	18
61	128	I	C	Н	P	L	Ř	Н	A	Т	v	18
62	134	Н	A	Т	V	L	T	L	P	R	v	18
63	154	G	A	A	L	М	Ā	Р	L	P	v	18
64	157	L	М	A	P	L	≏ P	V	F	I	K	18
65	190	A	C	D	D	I	R	V	N	v	V	18
66	229	G	L	Т	R	E	A	Q	A	K	A	18
67	245	Н	v	C	A	V	≏ F	I	F	Y	V	
		P	v					I				18
68	274 278		N	I	L	A	N		Y	L P	L	18
69		A	V		Y	L	Ē	V	P		V	18
70	291	I		Y	G	V	K	T	K	E	I	18
71	298	K	E	I	R	Q	<u>R</u>	I	L	R	L	18
72	48	I	Y	I	V	R	T	E	Н	S	L	17
73	65	L	C	M	L	S	G	I	D	I	L	. 17
74	67	M	L	S	G	Ι	\overline{D}	I	L	I	S	17
75	74	L	I	S	T	S	<u>s</u>	M	P	K	M	17
76	91	S	T	Т	Ι	Q	F	D	A	C	L	17
77	94	I	Q	F	D	A	<u>C</u>	L	L	Q	Ι	17
78	188	K	L	A	С	D	$\overline{\mathbf{D}}$, R	V	N	17
79	197	N	V	V	Y	G	<u>L</u>	Ι	V	Ι	I	17
80	200	Y	G	L	I	V	Ī	I	S	A	Ι	17
81	218	F	S	Y	L	L	Ī	L	K	T	V	17
82	227	V	L	G	L	Т	$\frac{R}{2}$	E	A	Q	A	17
83	303	R	I	L	R	L	<u>F</u>	H	V	A	Т	17
84	21	G	Г	E	Ē	A	Q	F	W	L	A	16
85	92	Т	T	Ι	Q	F	\overline{D}	A	С	L	L	16
86	97	D	A	С	L	L	Ō	Ι	F	A	Ι	16
87	127	A	Ι	С	Н	Р	$\bar{\Gamma}$	R	Н	A	Т	16
88	143	V	T	K	Ι	G	$\overline{\Lambda}$	A	A	v	V	16
89	195	R	V	N	V	V	<u>Y</u>	G	L	Ι	V	16
90	220	Y	L	L	Ι	L	$\underline{\mathbf{K}}$	Т	V	L	G	16
91	296	K	Т	K	E	Ι	R	Q	R	Ι	L	16
92	18	G	L	P	G	L	$\underline{\mathbf{E}}$	E	A	Q	F	15
93	30	Α	F	P	L	С	<u>s</u>	L	Y	L	Ι	15
94	126	V	A	Ι	C	Н	P	\mathbf{L}	R	H	А	15
95	145	K	I	G	V	A	$\underline{\underline{A}}$	V	V	R	G	15
96	173	S	N	Ι	L	s	$\underline{\underline{H}}$	S	Y	C	L	15
97	201	G	L	I	V	I	Ī	Ş	Α	I	G	15
98	208	Α	I	G	L	D	$\underline{\mathbf{s}}$	L	L	I	S	15
99	210	G	L	D	S	L	$\underline{\mathbf{L}}$	Ι	s	F	s	15
100	267	K	R	R	D	S	P	L	P	v	Ι	15
												31

HLA-A*0201 decamers(SEQ ID

NOS 2154-2253, respectively
in order of appearance)

Pos 1 2 3 4 5 6 7 8 9 0 score

HLA-A*0203 decamers(SEQ ID NOS 2254-2301, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	141	P	R	v	Т	K	Ι	G	V	A	Α	19
2	147	G	v	A	Α	V	V	R	G	A	Α	19
3	112	М	E	s	Т	V	L	L	Α	M	Α	18
4	227	V	L	G	L	Т	R	E	Α	Q	Α	18
5	229	G	L	T	R	E	A	Q	Α	K	Α	18
6	142	R	V	T	K	I	G	v	Α	A	V	17
7	148	v	A	A	V	V	R	G	Α	A	L	17
8	2	V	D	P	N	G	N	E	S	s	Α	10
9	16	, L	I	G	L	P	G	Ŀ	E	E	Α	10
10	21	G	L	E	E	Α	Q	F	W	L	Α	10
11	31	F	P	L	С	S	L	Y	L	I	Α	10
12	76	S	T	s	S	М	P	K	M	L	Α	10
13	89	F	N	s	Т	Т	Ι	Q	F	D	Α	10
14	96	F	$\overline{\mathbf{D}}$	A	С	\mathbf{L}	$_{\rm L}$	Q	Ι	F	Α	10
15	110	S	G	M	Ε	S	Т	V	L	L	Α	10
16	118	L	A	M	Α	F	D	R	Y	v	Α	10
17	126	V	A	I	C	Н	P	L	R	Н	Α	10
.18	140	L	P	R	V	Т	K	Ī	G	v	Α	10
19	146	I	G	v	Α	Α	V	V	R	G	Α	10
20	150	А	V	v	R	G	Α	A	L	M	Α	10
21	181	C	Ŀ	H	Q	D	V	M	K	L	A	10
22	199	V	Y	G	L	1	V	Ī	Ι	s	Α	10
23	225	K	T	v	L	G	L	$\underline{\mathbf{T}}$	R	E	Α	10
24	239	F	$\underline{\mathbf{G}}$	T	С	V	S	H	V	С	Α	10
25	269	R	$\underline{\mathbf{D}}$	s	P	L	Ρ	\underline{V}	Ι	L	Α	10
26	302	Q	R	I	\mathbf{L}	R	L	F	Н	v	Α	10
27	305	L	R	L	F	Н	V	A	Т	н	Α	10
28	3	Đ	P	N	G	N	E	\underline{s}	S	A	Т	9
29	17	I	$\underline{\mathbf{G}}$	L	P	G	L	E	E	A	Q	9
30	22	L	E	E	Α	Q	F	M	L	A	F	9
31	32	P	L	C	S	L	Y	Ī	I	A	V	9
32	77	Т	\underline{s}	s	M	P	K	$\underline{\underline{M}}$	L	A	Ι	9
33	90	N	$\underline{\underline{s}}$	T	Т	I	Q	F	D	A	С	9
34	97	D	A	С	L	L	Q	$\underline{\mathtt{I}}$	F	A	I	9
35	111	G	M	E	S	Т	V	Ē	L	A	М	9
36	113	E	\underline{s}	T	V	L	\mathbf{L}	A	М	A	F	9
37	119	Α	M	A	F	D	R	Y	V	A	Ι	9
38	127	Α	I	С	Н	P	\mathbf{L}	\underline{R}	Н	A	Т	9
39	151	V	$\underline{\mathtt{v}}$	R	G	A	A	$\underline{\mathtt{L}}$	M	A	P	. 9
40	182	L	$\overline{\mathbf{H}}$	Q	D	V	М	K	L	A	С	9
41	200	Y	\underline{G}	L	I	V	I	<u>I</u>	S	A	1	9
42	226	T	\underline{v}	L	G	L	T	R	E	A	Q	9
43	228	Γ	$\underline{\mathbf{G}}$	L	T	R	E	A	Q	A	K	9
												32

HLA-A*0203 decamers(SEQ ID NOS 2254-2301, respectively in order of appearance)

score	0	9	8	7	6	5	4	3	2	1	Pos	
9	F	A	K	A	Q	Α	E	R	T	L	230	44
9	V	A	C	V	Н	S	V	C	$\underline{\underline{\mathbf{T}}}$	G	240	45
9	N	A	L	I	V	P	L	P	\mathbf{S}	D	270	46
9	Т	A	V	$\overline{\mathbf{H}}$	F	L	R	L	Ī	R	303	47
9	S	Α	Н	Т	Α	V	Н	F	L	R	306	48

HLA-A26 decamers (SEQ ID NOS 2302-2366, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	299	E	Ι	R	Q	R	Ι	L	R	L	F	31
2	193	D	Ι	R	V	N	V	v	Y	G	L	29
3	250	F	Ι	F	Y	v	P	F	I	G	L	25
4	256	F	I	G	L	S	М	V	Н	R	F	25
5	74	L	Ι	s	Т	s	s	М	P	K	М	24
6	274	P	V	I	L	Α	N	Ι	Y	L	L	24
7	1.8	G	L	P	G	L	E	E	Α	Q	F	23
8	116	v	L	L	Α	М	Α	F	D	R	Y	23
9	205	I	I	S	A	Ι	G	L	D	S	L	23
10	221	L	L	I	L	K	Т	V	L	G	L	23
11	230	\mathbf{L}	Т	R	E	Α	Q	Α	K	Α	F	23
12	13	Y	F	Ι	L	Ι	G	\mathbf{L}	P	G	L	22
13	40	Α	V	L	G	N	L	Т	Ι	I	Y	22
14	56	S	L	Н	E	P	М	Y	I	F	L	22
15	95	Q	F	D	Α	С	L	L	Q	I	F	22
16	215	L	I	S	F	S	Y	\mathbf{L}	L	Ι	L	22
17	92	\mathbf{T}	T	I	Q	F	D	Α	C	L	L	21
18	100	L	L	Q	Ι	F	Α	I	Н	s	L	21
19	103	I	F	A	I	Н	S	L	S	G	М	21
20	296	K	T	K	E	1	R	Q	R	Ι	L	21
2,1	28	W	L	Α	F	P	\mathbf{L}	С	S	\mathbf{L}	Y	20
22	131	P	\mathbf{L}	R	H	Α	Т	V	L	Т	L	20
23	59	Е	P	М	Y	1	F	L	C	M	L	19
24	91	s	Т	T	Ι	Q	F	D	A	С	L	19
25	202	\mathbf{L}	Ι	V	Ι	I	S	A	1	G	L	19
26	212	D	S	L	L	Ι	S	F	S	Y	L	19
27	272	P	L	P	V	Ι	L	A	N	Ι	Y	19
28	279	N	Ι	Y	L	L	V	P	P	V	L	19
29	52	R	T	E	Н	S	\mathbf{L}	Н	E	P	М	18
30	62	Y	Ι	F	L	С	M	L	S	G	Ι	18
31	72	D	Ι	\mathbf{L}	Ι	S	T	S	S	M	Р	18
32	108	S	L	S	G	M	E	S	Т	V	L	18
33	113	E	S	T	V	L	L	A	М	A	F	18
34	151	V	V	R	G	A	A	L	M	A	P	18
35	78	s	S	M	P	K	M	L	A	I	F	17
36	142	R	V	Т	K	I	G	V	A	A	V	17
37	162	P	V	F	Ι	K	Q	L	P	F	С	17
38	164	F	Ι	K	Q	L	P	F	С	R	S	17
												33

HLA-A26 decamers(SEQ ID NOS 2302-2366, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score	
39	167	Q	L	P	F	С	R	S	N	I	L	17	
40	185	D	V	М	K	L	Α	C	D	D	1	17	
41	248	Α	V	F	Ι	F	Y	V	P	F	I	17	
42	253	Y	V	P	F	Ι	G	L	S	М	V	17	
43	45	$_{ m L}$	T	1	1	Y	Ι	V	R	Т	E	16	
44	145	K	I	G	٧	Α	A	V	V	R	G	16	
45	198	V	٧	Y	G	L	Ι	V	I	I	S	16	
46	203	I	V	Ι	Ι	S	Α	I	G	L	D	16	
47	209	I	G	L	D	S	L	L	1	S	F	16	
48	213	S	L	L	Ι	S	F	S	Y	L	L	16	
49	255	P	F	I	G	L	S	M	V	Н	R	16	
50	264	R	F	S	K	R	R	D	S	P	L	16	
51	294	G	V	K	Т	K	E	Ι	R	Q	R	16	
52	16	L	I	G	L	P	G	L	Е	Е	A	15	
53	80	M	Р	K	М	L	Α	Ι	F	W	F	15	
54	114	S	Т	V	L	L	A	M	Α	F	D	15	
55	155	A	A	L	M	A	P	L	P	V	F	15	
56	159	Α	P	L	P	V	F	Ι	K	Q	L	15	
57	174	N	Ι	L	S	H	S	Y	С	\mathbf{L}	Н	15	
58	197	N	V	V	Y	G	L	I	V	Ι	Ι	15	
59	210	G	L	D	S	L	\mathbf{L}	Ι	S	F	S	15	
60	214	L	L	Ι	S	F	S	Y	L	\mathbf{L}	I	15	
61	222	L	Ι	\mathbf{L}	K	T	V	L	G	\mathbf{L}	T	15	
62	240	G	Т	С	V	S	Н	V	С	A	V	15	
63	247	C	A	V	F	I	F	Y	٧	P	F	15	
64	286	P	V	L	N	P	Ι	V	Y	G	V	15	
65	298	K	E	Ι	R	Q	R	Ι	L	R	L	15	

HLA-A3 decamers (SEQ ID NOS 2367-2432, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	136	\mathbf{T}	v	$\overline{\mathbf{r}}$	T	L	$\underline{\mathtt{P}}$	R	V	T	K	31
2	287	V	L	$\overline{\mathbf{N}}$	P	I	$\overline{\Lambda}$	Y	G	V	K	28
3	223	I	L	$\underline{\mathtt{K}}$	T	V	$\overline{\mathbf{r}}$	$\underline{\mathbf{G}}$	L	T	R	27
4	304	I	L	$\underline{\mathtt{R}}$	L	F	$\underline{\mathbf{H}}$	\underline{v}	Α	T	H	27
5	73	I	L	Ī	s	Т	\underline{s}	S	М	P	K	26
6	15	I	L	Ī	G	L	P	$\underline{\underline{G}}$	L	E	E	23
7	40	Α	v	$\bar{\Gamma}$	G	N	$\underline{\mathbf{L}}$	$\underline{\mathbf{T}}$	I	I	Y	23
8	150	Α	v	\underline{v}	R	G	A	A	L	M	A	23
9	258	G	L	<u>s</u>	М	V	\overline{H}	$\underline{\mathbf{R}}$	F	S	K	23
10	18	G	L	P	G	L	E	E	A	Q	F	22
11	303	R	I	Ē	R	L	$\underline{\mathbf{F}}$	H	V	A	T	22
12	276	I	L	A	N	I	Y	$\overline{\mathbf{r}}$	L	v	P	21
13	28	W	L	A	F	Р	ഥ	\underline{C}	S	L	Y	20
14	115	Т	v	L	L	Α	M	A	F	D	R	20
15	116	V	L	$\underline{\mathtt{L}}$	Α	М	$\underline{\mathbf{A}}$	$\underline{\mathbf{F}}$	D	R	Y	20
16	125	Y	V	$\underline{\underline{A}}$	Ι	С	H	P	L	R	Н	20
17	131	P	L	$\underline{\mathbf{R}}$	Н	Α	$\underline{\underline{\mathbf{T}}}$	V	L	T	L	20
18	144	\mathbf{T}	K	I	G	V	A	A	V	v	R	20
												34

HLA-A3 decamers (SEQ ID NOS 2367-2432, respectively in order of appearance)

	Pos 1234567890												
	Pos	1	2	3	4	5	6	7	8	9	0	score	
19	156	Α	L	M	А	Ρ	Ī	P	V	F	Ι	20	
20	195	R	v	N	V	V	Y	G	L	I	V	20	
21	35	S	L	$\underline{\mathbf{Y}}$	L	Ι	A	V	L	G	N	19	
22	272	P	L	P	V	1	L	A	N	I	Y	19	
23	37	Y	L	1	Α	v	L	G	N	L	Т	18	
24	49	Y	I	v	R	\mathbf{T}	E	Н	s	L	Н	18	
25	50	I	v	R	Т	E	H	s	L	н	Е	18	
26	108	S	L	s	G	M	E	s	Т	v	L	18	
27	142	R	v		K	I	G	v	Α	A	v	18	
28	188	К	L	A	С	D	D	I	R	v	N	18	
29	279	N	I	Y	L	L	v	P	P	v	L	18	
30	291	I	v	Y	G	V	K	T	K	E	I	18	
31	294	G	v	K	Т	K	E	I	R	Q	R	18	
32	46	т	I	Ī	Y	I	v	R	Т	E	Н	17	
33	102	Q	I	F	Α	I	H	s	L	s	G	17	
34	151	v	v	R	G	Α	Ā	L	М	Α	Р	17	
35		S	Y	C	L	Н	Q	D	v	М	K	17	
36		I	v	ī	I	s	~ A	I	G	L	D	17	
37		v	I	ĭ	s	A	I	G	L	D	S	17	
38		Y	L	L	I	L	ĸ	T	v	L	G	17	
39		L	L	I	L	K	T	v	L	G	L	17	
40		v	L	Ğ	L	Т	R	Ē	A	Q	A	17	
41		C	v	S	Н	v	C	= A	v	F	I	17	
42		N	P	ĭ	v	Y	Ğ	v	ĸ	T	K	17	
43		L	I	Ä	v	L	G	Ņ	L	T	I	16	
44		A	I	F	W	F	N	S	Т	т	I	16	
45		G	v	Ā	A	v	v	R	G	A	Ā	16	
46		v	v	Y	G	L	ĭ	v	I	I	s	16	
47		G	L	Ī	V	I	Ī	š	A	I	G	16	
48		L	L	Ī	s	F	s	Y	ь	L	Ι	16	
49		Т	v	L	G	L	T	R	E	A	Q	16	
50		Ŀ	G	L	Т	R	Ė	A	Q	A	K	16	
51		G	L	T	R	E	_		A	ĸ	A	16	
52		M	v	D	P	N	A G	Й	E	s	s	15	
53		N	L	T	I	I	Y	I	v	R	Т	15	
54		I	I	Y	I	v	R	T	E	н	s	15	
55		M	L	s	G	I	D	i	L	ı	s	15	
		D	I		I	s			S	м	P	15	
56 57		C	L	<u>L</u>		I	T	<u>s</u>	I	Н	S	15	
				H F	Q		F	A	М	E	S	15	
58		A			S	L	S	G					
59		K		G	V	A	A	V	V	R	G	15 15	
60		I	L	<u>S</u>	H	S	<u>Y</u>	C	L	H	Q	15	
61		C	D	D	Ι	R	V	N	V	V	Y	15	
62		A		G	L	D	<u>s</u>	<u>L</u>	L	I	S	15	
63		V	I	L	A	N	Ī	<u>Y</u>	L	L	ν	15	
64		Y	L	Ŀ	V	P	P	V	L	N	P	15	
65		E	I	R	Q	R	Ī	<u>L</u>	R	L	F	15	
66	306	R	L	F	Н	V	A	$\underline{\mathbf{T}}$	H	A	S	15	

HLA-B*0702 decamers (SEQ ID

NOS 2433-2492, respectively in order of appearance)

in order of appearance)												
	Pos	1	2	3	4	5	6	7	8	9	0	score
1	159	A	P	L	P	V	F	Ι	K	Q	L	23
2	59	E	P	М	Y	Ι	F	L	C	M	\mathbf{L}	22
3	273	L	P	V	Ι	L	Α	N	I	Y	L	20
4	3	D	P	N	G	N	E	S	S	A	Т	19
5	130	Н	P	L	R	Н	Α	Т	V	L	Т	19
6	140	L	P	R	v	T	K	Ι	G	v	Α	19
7	161	L	P	v	F	Ι	K	Q	L	P	F	19
8	31	F	P	L	С	S	L	Y	L	I	Α	18
9	271	S	P	L	P	v	I	L	Α	N	Ι	18
10	80	М	P	К	М	L	Α	I	F	w	F	16
11	108	s	L	s	G	М	E	S	Т	v	L	16
12	131	P	L	R	Н	Α	Т	V	L	т	ь	15
13	264	R	F	s	K	R	R	D	s	P	L	15
14	33	L	C	s	L	Y	L	I	A	v	L	14
15	109	L	s	G	М	Ē	s	Т	v	L	L	14
16	152	v	R	G	Α	A	L	M	A	P	L	14
17	205	I	ı	s	Α	I	G	L	D	s	L	14
18	215	L	I	S	F	s	Y	L	L	I	L	14
19		R	R	D	s	P	L	Р	V	I	L	14
							С				L	13
20		L	A	F A	P	L	R	S	L A	Y A	L	13
21	148	V	A		V	Λ		G				
22	156	A		M	A	P	L	P	V	F	I	13
23		D		R	V	N	V	V	Y	G	L	13
24		L		I	L	K	Т	V	L	G	L	13
25		K		Ι	R	Q	R	Ι	L	R -	L	13
26				S	S	A	T	Y	F	I	L	12
27		L		G	L	Ε	Ē	A	Q	F	W	12
28		E	Α	Q	F	W	L	A	F	P	L	12
29				A	F	D	R	Y	V	A	Ι	12
30				P	L	R	Н	A	Т	V	L	12
31			S	A	Ι	G	L	D	S	L.		12
32				\mathbf{L}	L	1	L	K	Т	V	L	12
33			Ι	Y	L	L	V	₽	Ρ	V	L	12
34	285	P		V	L	N	P	Ι	V	Y	G	12
35	8	E	S	S	A	Т	Y	F	1	L	Ι	11
36	13	Y	F	Ι	L	Ι	G	L	P	G	L	11
37	27	F	W	L	A	F	Ρ	L	С	S	L	11
38	48	I	Y	I	V	R	Т	E	Н	S	L	11
39			L	Н	Ε	P	М	Y	Ι	F	L	11
40	65	L	C	M	L	S	G	Ι	D	I	L	11
41	. 75	I	S	Т	S	S	M	P	K	M	L	11
42	77	Γ	S	S	М	P	K	М	L	A	Ι	11
43	91	S	Т	\mathbf{T}	Ι	Q	F	D	Α	C	L	11
44	123	D	R	Y	V	Α	Ι	С	Н	P	L	11
45	142	R	v	Т	K	Ι	G	V	A	Α	V	11
46	180	Y	C	L	Н	Q	D	V	Μ	K	L	11
47	190	A	C	D	D	1	R	V	N	v	V	11
48	212		s	L	L	I	S	F	S	Y	L	11
49		A	Q	Α	K	Α	F	G	Т	С	V	11
50	242			S	Н	V	С	Α	V	F	Ι	11
51					Ι	F	Y	v	Р	F	I	11
												36
												_ •

HLA-B*0702 decamers (SEQ ID NOS 2433-2492, respectively in order of appearance) Pos 1 2 3 4 5 6 7 8 9 0 score F I F Y V P F I G L 52 250 11 53 254 V P F I G L S M V H 11 54 266 SKRRDSPL**P**V 11 55 267 KRRDSPLPVI 11 RDSPLPVILA 56 269 11 57 278 ANIYLLVPPV 11 58 284 V P P V L N P I V Y 11 N P I V Y G V K T K 59 289 11 60 296 KTKEIRQRIL 11

Please replace Table XXVIII, beginning at page 205, line 1, with the following rewritten

Table XXVIII:

-- Table XXVIII:

HLA Class II Epitopes (sample 15-mer length)

(SEQ ID NOS 2493-2595, respectively in order of appearance) HLA-DRB1*0101 15-mers

	Pos	-	_	_		_	_	-	_	_	^	,	_	2	4	5	score
-	200	1	2	3	4	5	6	7	8	9			2			_	2.6
1	200	Y	G	L	Ι	V	I	Ι	S	A	Ι	G	L	D	S	L	36
2	68	L	S	G	I	D	I	L	Ι	S	Т	S	S	M	P	K	34
3	62	Y	Ι	F	L	C	M	L	S	G	I	D	I	L	I	S	33
4	103	I	F	Α	I	H	S	L	S	G	М	Ε	S	\mathbf{T}	V	\mathbf{L}	32
5	45	L	\mathbf{T}	Ι	I	Y	I	V	R	T	E	Н	S	L	H	E	31
6	193	D	Ι	R	V	N	V	V	Y	G	L	I	V	Ι	I	S	31
7	277	L	Α	N	I	Y	L	L	V	P	Р	V	L	N	P	Ι	31
8	97	D	Α	C	L	L	Q	Ι	F	A	I	Η	s	L	S	G	30
9	106	I	H	S	L	S	G	М	E	S	Т	V	L	L	Α	M	30
10	240	G	Т	С	v	S	H	V	С	A	V	F	I	F	Y	V	30
11	10	s	Α	\mathbf{T}	Y	F	I	L	I	G	L	P	G	L	E	E	29
12	289	N	Ρ	1	v	Y	G	V	K	T	K	E	Ι	R	Q	R	29
13	11	A	\mathbf{T}	Y	F	I	L	Ι	G	L	P	G	L	E	Е	Α	28
14	250	F	Ι	F	Y	V	P	F	I	G	L	s	М	V	H	R	27
15	140	L	Ρ	R	v	\mathbf{T}	K	Ι	G	v	Α	A	V	V	R	G	26
16	183	н	Q	D	v	М	ĸ	L	Α	C	D	D	Ι	R	V	N	26
17	217	s	F	S	Y	L	L	I	L	ĸ	Т	V	L	G	L	Т	26
18	16	L	Ι	G	L	P	G	L	E	E	Α	Q	F	W	L	Α	25
19	24	E	Α	Q	F	W	L	Α	F	P	L	С	S	L	Y	L	25
20	36	L	Y	L	I	Α	v	L	G	N	\mathbf{L}	\mathbf{T}	Ι	I	Y	Ι	25
21	70	G	I	D	I	L	I	S	\mathbf{T}	s	s	М	Р	K	М	L	25
22	111	G	М	E	s	Т	v	L	L	Α	М	Α	F	D	R	Y	25
23	148	v	Α	Α	v	V	R	G	Α	A	L	М	Α	Р	L	P	25
24	162	P	V	F	I	K	Q	L	Р	F	С	R	s	N	I	L	25
25	197	N	V	V	Y	G	L	I	V	I	I	s	Α	I	G	L	25
26	211	L	D	s	L	L	r	s	F	s	Y	L	L	Ι	L	K	25

HLA-DRB1*0101 15-mers

Pos										_						score
	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	
27 218	F	S	Y	L	L	I	L	K	T	V	L	G	L	Т	R	25
28 13	Y	F	Ι	L	Ι	G	L	P	G	L	E	E	A	Q	F	24
29 30	Α	F	P	L	C	S	L	Y	L	Ι	A	V	L	G	N	24
30 39	Ι	A	V	L	G	N	L	Т	I	I	Y	1	V	R	Т	24
31 77	Т	S	S	М	Р	K	M	L	A	Ι	F	M	F	N	S	24
32 85	A	I	F	W	F	N	S	Т	T	Ι	Q	F	D	A	C	24
33 137	V	L	Т	L	Р	R	V	Т	K	Ι	G	V	Α	A	V	24
34 151	V	V	R	G	A	A	L	M	A	P	L	P	٧	F	1	24
35 161	L	P	V	F	I	K	Q	L	P	F	C	R	S	И	I	24
36 196	v	N	V	V	Y	G	L	I	V	I	Ι	S	A	I	G	24
37 202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	24
38 208	A	Ι	G	L	D	S	L	Г	I	S	F	S	Y	L	L	24
39 248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	24 24
40 251	1	F	Y	v	P	F	Ι	G	L	S	M	V	H	R	F	23
41 83	M	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	23
42 101 43 165	L	Q	I	F	A	I	Н	S	L	S	G	M	E	S	T	23
44 203	I	K V	Q	L	P	F	С	R G	S	N	Ι	L	S	H	S	23
45 221		v L	I	I L	S K	A T	I V	L	L	D D	S	L R	L E	I A	S	23
46 278	L A	И	I	Y	L	L	V	Р	G P	V	L	N	E. P	I	Q V	23
47 27	F	M	L	A	F	Р	v L	C	S	v L	Y	L	I	A	V	22
48 35	s	L	Y	L	I	A	Λ	L	G	И	L	Т	I	I	Y	22
49 61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	22
50 65	L	C	М	L	S	G	I	D	I	L	I	S	T	S	s	22
51 80	м	P	K	м	L	A	I	F	W	F	И	S	Т	T	I	22
52 145	K	I	G	v	A	A	V	V	R	G	A	A	L	М	Ā	22
53 146	I	G	V	A	A	v	V	R	G	A	Α	L	М	Α	P	22
54 154	G	A	Ā	L	М	A	P	L	P	V	F	I	K	Q	L	22
55 205	I	I	S	A	I	G	L	D	s	L	L	I	s	F	s	22
56 243	v	s	Н	v	Ċ	A	v	F	I	F	Y	v	P	F	I	22
57 270	D	s	P	L	P	v	I	L	A	N	I	Y	L	L	v	22
58 274	P	v	I	L	A	N	I	Y	L	L	v	P	P	v	L	22
59 281	Y	L	L	v	P	P	v	L	N	P	I	v	Y	G	v	22
60 34	C	S	L	Y	L	I	Α	V	L	G	N	L	т	·I	I	21
61 69	S	G	Ι	D	Ι	L	Ι	s	т	s	S	М	Р	K	Μ	21
62 152	v	R	G	Α	Α	L	М	Α	P	L	Р	V	F	Ι	K	21
63 299	E	Ι	R	Q	R	I	L	R	L	F	Н	V	Α	т	Н	21
64 100	L	L	Q	I	F	Α	I	Н	s	L	s	G	М	E	S	20
65 135	A	Т	V	L	\mathbf{T}	L	Р	R	v	Т	K	Ι	G	V	Α	20
66 141	P	R	V	T	K	I	G	V	A	Α	V	V	R	G	Α	20
67 191	C	D	D	I	R	v	N	V	v	Y	G	L	I	V	I	20
68 199	v	Y	G	L	I	v	I	I	s	Α	I	G	L	D	S	20
69 262	v	Н	R	F	S	K	R	R	D	s	Р	L	P	V	Ι	20
70 271	S	P	L	P	V	I	L	Α	N	I	Y	L	L	V	P	20
71 28	W	L	Α	F	P	L	C	S	L	Y	L	I	Α	V	L	19
72 58	H	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	19
73 59	E	P	M	Y	I	F	L	C	M	L	S	G	Ι	D	Ι	19
74 60	P	M	Y	I	F	L	С	M	L	S	G	Ι	D	Ι	L	19
75 98	A		L	L	Q	I	F	A	I	Η	S	L	S	G	M	19
76 215	L	I	S	F	S	Y	L	L	I	L	K	T	V		G	19
77 219	S	Y	L	L	Ι	L	K	T	V	L	G	L		R	E	19
													3	38		

HLA-DRB1*0101 15-mers

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
78	228	L	G	L	т	R	E	Α	Q	A	K	Α	F	G	Т	С	19
79	232	R	E	Α	Q	Α	ĸ	Α	F	G	Т	C	V	S	Н	V	19
80	246	v	С	Α	v	F	I	F	Y	v	P	F	1	G	L	s	19
81	297	T	K	E	I	R	Q	R	Ι	L	R	L	F	Н	V	Α	19
82	3	D	P	N	G	N	E	S	s	A	\mathbf{T}	Y	F	I	L	Ι	18
83	14	F	I	\mathbf{L}	I	G	L	P	G	L	E	E	Α	Q	F	W	18
84	25	Α	Q	F	W	L	A	F	P	L	C	S	L	Y	L	Ι	18
85	42	L	G	N	L	T	I	I	Y	I	V	R	Т	Е	H	s	18
86	46	Т	I	I	Y	I	V	R	Т	E	Η	S	L	H	Е	Р	18
87	78	S	S	М	P	K	M	L	A	I	F	W	F	N	S	Т	18
88	84	L	A	Ι	F	W	F	N	S	T	\mathbf{T}	Ι	Q	F	D	A	18
89	89	F	N	S	T	\mathbf{T}	I	Q	F	D	A	C	L	L	Q	Ι	18
90	93	T	Ι	Q	F	D	A	С	L	L	Q	Ι	F	A	Ι	Н	18
91	115	T	V	L	L	A	M	A	F	D	R	Y	V	A	Ι	C	18
92	119	A	М	А	F	D	R	Y	V	A	Ι	C	H	P	L	R	18
93	127	A	I	C	H	Р	L	R	Η	Α	Т	V	L	Т	L	Р	18
94	129	C	H	P	L	R	Н	Α	\mathbf{T}	-	L	Т	L	Р	R	V	18
95	147	G	V	A	. A	V	V	R	G	A	Α	L	М	A	Р	\mathbf{L}	18
96	149	Α	A	V	v	R	G	A	A	L	M	A	Р	Г	Р	V	18
97	216	I	S	F	S	Y	L	. Г	Ι	L	K	Т	V	L	G	L	18
98	227	V	L	G	L	\mathbf{T}	R	E	A	Q	A	K	Α	F	G	Т	18
99	249	V	F	I	F	Y	v	Р	F	I	G	L	S	М	V	Н	18
100	253	Y	V	Ρ	F	Ι	G	L	S	M	V	Н	R	F	S	K	18
101	284	V	P	P	v	L	N	P	Ι	V	Y	G	V	K	Т	K	18
102	286	P	V	\mathbf{L}	N	Р	Ι	V	Y	G	V		Т	K	E	Ι	18
103	303	R	1	L	R	L	F,	H	V	Α	Т	H	A	S	E	P	18

HLA-DRB1*0301 (DR17) 15-mers (SEQ ID NOS 2596-2671, respectively in order of appearance)

P	os	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	26
2 2	06	I	s	A	I	G	L	D	s	L	L	I	s	F	S	Y	23
3	91	s	Т	\mathbf{T}	I	Q	F	D	Α	С	L	\mathbf{L}	Q	Ι	F	Α	22
4 1	17	L	L	A	M	A	F	D	R	Y	V	Α	Ι	C	Н	Р	22
5	38	L	I	Α	v	L	G	N	L	T	I	I	Y	I	V	R	21
6 1	79	s	Y	C	L	Н	Q	D	V	M	K	L	Α	С	D	D	21
7 2	11	L	D	S	L	L	I	s	F	s	Y	L	L	Ι	L	K	21
8 2	19	s	Y	L	L	I	L	K	\mathbf{T}	v	L	G	L	\mathbf{T}	R	E	21
9 2	72	P	L	P	v	I	L	Α	N	I	Y	L	\mathbf{L}	V	Р	P	21
10	26	Q	\mathbf{F}	W	L	Α	F	P	L	C	S	L	Y	L	Ι	Α	20
11 1	14	s	Т	V	L	L	A	М	Α	F	D	R	Y	V	Α	I	20
12 1	.29	C	Н	P	L	R	Н	Α	\mathbf{T}	v	L	Т	L	P	R	V	20
13 1	.34	н	Α	\mathbf{T}	v	L	T	L	P	R	V	Т	K	I	G	V	20
14 1	86	v	M	K	L	Α	C	D	D	I	R	V	N	V	V	Y	20
15 2	00	Y	G	L	I	V	I	Ι	s	A	Ι	G	L	D	S	L	20
16 2	270	D	s	P	L	P	v	Ι	\mathbf{L}	A	N	I	Y	L	L	V	20
17 2	97	T	K	E	I	R	Q	R	I	L	R	\mathbf{L}	\mathbf{F}	Н	V	Α	20
18	11	A	Т	Y	F	I	L	I	G	L	P	G	L	E	E	Α	19
19	54	E	Н	s	L	Н	E	P	М	Y	Ι	F	L	С	М	L	19
														3	39		

HLA-DRB1*0301 (DR17) 15-mers (SEQ ID NOS 2596-2671, respectively in order of appearance)

Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score
20 106	IHSLSGMESTVLLAM	19
21 165	IKQLPFCRSNILSHS	19
22 191	CDDIRVNVVYGLIVI	19
23 203	IVIISAIGLDSLLIS	19
24 213	SLLISFSYLLILKTV	19
25 224	LKTVLGLTREAQAKA	19
		19
		19
27 248		19
28 254		19
29 277		18
30 36	LYLIAVLGNLTIIYI	18
31 93	TIQFDACLLQIFAIH	18
32 98	ACLLQIFAIHSLSGM	
33 1,25	YVAICHPLRHATVLT	18
34 158	MAPLPVFIKQLPFCR	18
35 187	M K L A C D D I R V N V V Y G	18
36 217	SFSYLLILKTVLGLT	18
37 225	KTVLGLTREAQAKAF	18
38 281	YLLVPPVLNPIVYGV	18
39 288	LNPIVYGVKTKEIRQ	18
40 18	GLPGLEEAQFWLAFP	17
41 44	NLTIIYIVRTEHSLH	17
42 145	KIGVAAVVRGAALMA	17 17
43 159	APLPVFIKQLPFCRS	17
44 256	FIGLSMVHRFSKRRD	
45 259	LSMVHRFSKRRDSPL	17
46 137	V L T L P R V T K I G V A A V	16
47 262	V H R F S K R R D S P L P V I	16
48 294	GVKTKEIRQRILRLF	16
49 46	TIIYIVRTEHSLHEP	15
50 51	V R T E H S L H E P M Y I F L	15
51 172	RSNILSHSYCLHQDV	15
52 189	L A C D D I R V N V V Y G L I	15 15
53 212	D S L L I S F S Y L L I L K T	
54 218	FSYLLILK T VLGLTR	15 15
55 271	SPLPVILANIYLLVP	
56 279	NIYLLVPPVLNPIVY	15 14
57 12	TYFILIGLPGLEEAQ	14
58 35	SLYLIAVLGNLTIIY	14
59 64	F L C M L S G I D I L I S T S	14
60 140	L P R V T K I G V A A V V R G	14
61 273	LPVILANIYLLVPPV	
62 301	RQRILRLFHVATHAS	14
63 13	Y F I L I G L P G L E E A Q F	13
64 47	IIYIVRTEHSLHEPM	13 13
65 71	I D I L I S T S S M P K M L A	
66 80	MPKMLAIFWFNSTTI	13
67 109		13
68 113	ESTVLLAMAFDRY V A	13
	40	

HLA-DRB1*0301 (DR17) 15-mers (SEQ ID NOS 2596-2671, respectively in order of appearance)

τ	os																score
	· OS	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	
69	135	А	\mathbf{T}	V	L	\mathbf{T}	L	Ρ	R	v	\mathbf{T}	K	I	G	V	A	13
70	195	R	V	N	v	V	Y	G	L	I	V	Ι	I	S	Α	Ι	13
71 2	202	L	Ι	V	I	I	s	Α	I	G	L	D	S	L	L	Ι	13
72 :	220	Y	L	L	I	L	ĸ	\mathbf{T}	V	L	G	L	\mathbf{T}	R	Ē	Α	1.3
73 :	221	L	L	I	L	K	T	V	L	G	L	\mathbf{T}	R	E	Α	Q	13
74	264	R	F	s	ĸ	R	R	D	S	P	L	Р	V	I	L	Α	13
75	280	I	Y	L	L	V	P	Р	V	L	N	P	I	V	Y	G	13
76	302	0	R	Ι	L	R	L	F	Н	v	Α	Т	Н	Α	S	E	13

HLA-DRB1*0401 (DR4Dw4) 15-mers (SEQ ID NOS 2672-2805, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	36	L	Y	L	I	A	v	L	G	N	L	T	I	I	Ŷ	Ι	26
2	45	L	T	I	I	Y	I	v	R	T	E	Н	s	L	H	E	. 26
3	68	L	s	G	I	D	ī	L	I	s	T	s	s	M	P	K	26
4	83	M	L	A	I	F	w	F	N	s	\mathbf{T}	T	I	Q	F	D	26
5	134	н	A	т	v	L	т	L	Р	R	v	Т	K	ī	G	V	26
6	145	ĸ	I	G	v	Α	Α	v	v	R	G	Α	Α	L	M	Α	26
7	224	L	K	\mathbf{T}	v	L	G	L	\mathbf{T}	R	E	Α	Q	А	K	Α	26
8	227	v	L	G	L	Т	R	E	Α	Q	Α	K	Α	F	G	\mathbf{T}	26
9	256	F	Ι	G	L	s	М	v	Н	R	F	S	K	R	R	D	26
10	281	Y	L	L	v	P	P	v	L	N	Р	Ι	V	Y	G	V	26
11	289	N	Р	I	v	Y	G	v	K	T	K	E	I	R	Q	R	26
12	301	R	Q	R	I	\mathbf{L}	R	L	F	н	V	Α	\mathbf{T}	Н	A	S	26
13	11	A	Т	Y	F	1	L	I	G	L	P	G	L	E	E	А	22
14	24	E	Α	Q	F	W	L	A	F	P	L	C	S	L	Y	L	22
15	25	A	Q	F	W	L	A	F	Ρ	L	C	S	\mathbf{L}	Y	L	Ι	22
16	34	C	S	L	Y	L	I	A	V	L	G	N	L	Т	1	Ι	22
17	84	L	A	I	F	M	F	N	S	T	\mathbf{T}	Ι	Q	F	D	A	22
18	122	F	D	R	Y	V	A	I	C	Н	P	L	R.	H	Α	Т	22
19	197	N	. A	V	Y	G	L	I	V	I	I	S	A	I	G	\mathbf{L}	22
20	215	L		S	F	S	Y	L	L	I	L	K	Т	V	L	G	22
21	217	S			Y	L	L	I	L	K	Т	V	L	G	L	T	22
22	250	F		F	Y	V	P	F	1	G	L	S	M	V	H	R	22
23	278	A			Y	L	L	v	Р	P	V	L	N	P	Ι	V	22
24	19	I		_	L	E	E	A	Q	F	W	L	A	F	P	L	20
25	30	Æ			L	C	S	L	Y	L	I	A	V	L	G	N	20
26	33	I			L		L	I	A	V	L	G	N	L	T	Ι	20 20
27	35						A			G	И	L	T	I	Ι	Y	20
28	39					G	N		T	I	I	Y	I	V	R	T	20
29	42						I	I	Y	I	V	R	T	E	H	S	.20
30	44			_		I	Y		V		T	E	H	S	L M	H	.20
31	48		_		V		_	E	H L		L M	H L	E S	P G	I	Y D	20
32 33	58							F		G		D	I	L	I	S	20
34	62 65					_		_	-		L	I	S	Т	S	S	20
35	65 71					_	S			s	М		K	M	L	A	20
23	, 1		. г	, т	ш	1	3	1	ت	3	1-1	r	IX		41	^	20
														-	A T		

HLA-DRB1*0401 (DR4Dw4) 15-mers (SEQ ID NOS 2672-2805, respectively in order of appearance)

Pos	3 ,	_	_		_ ,		, ,		9 ()	1	2	3 ,	4	5	score	
26 0	1	2	3	4				-							I	20	
36 8		Р	K	M											Q	20	
37 8		K	M	Г	-							_			Q A	20	
38 9		Т	T	I	~											20	
39 9	_	Α	С	L		~						_			G		
40 9	8 A	C	Ь	L											M	20	
41 10	0 r	L	Q	Ι	F.									E	S	20	
42 10	3 I	F	Α	I		S I								V	L	20	
43 10	6 I	H	\mathbf{s}	L	S	G 1	M	E						A	M	20	
44 11	5 T	V	L	L	A :	M .	A	F:			Y		Α	I	C	20	
45 11		L	Α	M	Α	F :	D	R '	Y	V	A			H	P	20	
46 12	5 Y	V	Α	I	C	H	P	L :	R.	H	A	Т	V	L	Т	20	
47 12	9 c	Н	P	L	R	H.	A	T	V	L	Т	L	Ρ	R	V	20	
48 13	7 v	L	Т	L	P	R	V	\mathbf{T}	K	Ι	G	V	Α	Α	V	20	
49 14	0 L	P	R	v	T	K	I	G	V	Α	Α	V	V	R	G	20	
50 15	5 A	A	L	M	A	P	L	P	V	F	I	K	Q	L	P	20	
51 16	2 P	V	F	I	K	Q	L	Р	F	C	R	S	N	I	L	20	
52 16	55 I	K	Q	L	P	F	C	R	S	N	I	L	S	Н	S	20	
53 17	'9 s	Y	C	L	Н	Q	D	V	M	K	L	Α	С	D	D	20	
54 18	3 н	: Q	D	v	M	K	L	Α	C	D	D	I	R	V	N	20	
55 18	86 v	M	K	L	Α	C	D	D	I	R	V	N	V	V	Y	20	
56 19	93 D	I	R	v	N	v	v	Y	G	L	I	V	I	I	S	20	
57 19	96 v	N	V	v	Y	G	L	I	v	Ι	Ι	S	Α	1	G	20	
58 19	99 v	Y	G	L	Ι	V	I	I	s	Α	I	G	\mathbf{L}	D	S	20	
59 20)O Y	G	L	I	V	I	I	S	Α	I	G	L	D	S	L	20)
60 20	02 I	ı	V	I	I	s	A	1	G	L	D	s	L	\mathbf{L}	Ι	20)
61 2	03 1	: v	I	I	S	A	I	G	L	D	s	L	\mathbf{L}	Ι	S	20)
62 2	06 I	: s	A	I	G	L	D	S	L	L	I	s	F	S	Y	20)
63 2	08 2	I	G	L	D	s	L	L	I	S	F	S	Y	\mathbf{r}	L	20)
64 2	11 I	ı D	S	L	\mathbf{L}	I	S	F	S	Y	L	L	1	L	K	20)
65 2	12 I) S	L	L	Ι	S	F	S	Y	\mathbf{L}	L	I	L	K	\mathbf{T}	20)
66 2	18 E	9	SY	L	L	I	L	K	T	V	L	G	L	Т	R	20)
67 2	40	T	. C	v	S	H	v	С	A	V	F	Ι	F	Y	V	20)
68 2	43 \	7 5	B	v	C	A	v	F	I	F	Y	V	Ρ	F	1	20)
69 2	46 \	7 (P	v	F	I	F	Y	v	P	F	I	G	L	S	20)
70 2	48 2	I A	/ F	' I	F	Y	v	P	F	I	G	L	S	M	V	20)
71 2	51	E F	Y	v	P	F	I	G	L	S	M	V	Н	R	F	20)
72 2	72 I	? I	Ē	v	Ι	L	A	N	I	Y	\mathbf{L}	L	V	P	P	20	Э
73 2	77 J	L A	A N	I	Y	L	L	V	P	P	V	L	N	P	Ι	20	Э
74 2	85 1	P 1	<i>]</i>	7 L	N	P	I	V	Y	G	V	K	Т	K	E	20	0
75	18 (3 I	. E	G	L	E	E	Α	Q	F	W	L	A	F	Р	18	
76	27	F V	N I	A	F	P	L	C	S	L	Y	L	Ι	Α	V	18	8
77	69	s (3]	[E	I	L	I	S	T	S	S	M	P	K	M		
78	94	I (Q F	F) A	C	L	L	Q	I	F			H			
79	99	C J	LI	. Č) I	F	A	I	Н	S	\mathbf{L}	S	G	M			
80 1	.07	н :	s I	ີ 5	G	M	E	S	T	V	L	L	A	M	Α		
81 1	.16	v :	L I	. A	M	A	F	D	R	Y	V	Α	I	C	H		
82 1	26	V A	A :	Ι (: н	P	L	R	H			V	L				
83 1	.64	F :	I	Κ 🕻	L	P	F	С	R	S	N						
84 1	.76	L	S I	H S	Y	C	L	Н	Q	D	V	M				. 1	8
														42			

HLA-DRB1*0401 (DR4Dw4) 15-mers (SEQ ID NOS 2672-2805, respectively in order of appearance)

P	os	1 :	2 3	3 4	5	6	7	8	9	0	1	2	3	4	5	5	score
O.E.	187			À		D	D	I	R	V		v	ν	Y	. (3	18
85				5 A		G	L	D	s	L						3	18
86	205					A	F	G	Т	C						7	18
87	233			~				S	н	ν						I	18
88	237			FG -		C	V									P P	18
89	271			L F		I	L	A	N								18
90	293			V K		K	E	Ι	R							[[
91	294	G	V :	K 1			I	R	Q							F	18
92	10	s	Α '	Τ 3	F	I	L	Ι	G							E	16
93	28	W	L.	A I	P	L	C	S	L							L	16
94	59	E	Р	M 3	ľ	F	L	C	M	Ι	. 5	3 (3]			Ι	16
95	61	M	Y	I	L	C	M	L	S	C	3]	ΙΙ)]	[I		Ι	16
96	85	A	Ι	F V	₹ F	N	S	Т	T	.]	ζ) I	7 [) [1	C	16
97	101	L	Q	I 1	P	I	Н	S	I		3 (3 1	1 I	3 5	3	Т	16
98	177	s	Н	s :	7 C	L	н	Q	E	7	<i>7</i> 1	1 I	()	. <i>1</i>	4	C	16
99	236	A	K	A 1	e c	T	· C	. v	· S	; F	1 I	J	2 7	I E	J	F	16
100	249	V	F		e y		P	F	, 1	: (3 1	L 5	3 6	v Iv	V	Н	16
101	253	Y	v		F 3			S	·	ſ	J	H	2]	F S	3	K	16
102	13	Y	F		 L]							E]	E 2	A (2	F	14
102	14	F	I		I										F	W	14
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104	16		I		v I							-			V	R	14
105	38	L	I			/ F									P	M	14
106	47	I				, r									M	L	14
107	54	E	H												I	L	14
108	60	P	M			? I									T	s	14
109	64	F	L			և Տ									M	L	14
110	70	G	I	D			[5								A	I	14
111	72	D	Ι	L													14
112	109	L	S				-								F	D	14
113	113	E	S	T									R		V	A	
114	135	A	T	V								K	I		V	A	14
115	143	V	Т	K								R	G		A	L	14
116	148	v	Α	Α	V	V I	R (G Z	Α.	A		М	A	P	L	P	14
117	149	A	Α	V	V	R (G Z	Α.		L	M	A	P	L	Р	V	14
118	154	G	Α	Α	L	Μ.	A :	P	L	P	V	F	Ι	K	Q	L	14
119	158	M	Α	P	L	Ρ.	V :	F	I	K	Q	L	P	F	C	R	
120	173	s	N	I	L	S	H	S	Y	С	L	H	Q	D	V	M	
121	184	Q	D	V	M	K	L.	A	C	D	D	Ι	R	V	N	V	
122	191	С	D	D	I	R	v :	N	V	V	Y	G	Ŀ	Ι	V	I	14
123	195	R	v	N	v	V	Y	G	L	I	V	Ι	Ι	S	A	Ι	
124	213	S	L	L	I	s	F	S	Y	L	L	Ι	L	K	T	V	14
125		Y	. Г	L	I	L	K	T	V	L	G	L	Т	R	E	A	14
126		L	L	Ι	L	K	т	v	L	G	L	T	R	E	Α	Q	14
127		K			L	G	L	т	R	E	Α	Q	Α	K	Α	F	14
128		I			v			F	S	ĸ	R	R	D	S	P	I.	, 14
129		ľ			L		v	I	L	Α	N	1	Y	L	L	V	7 14
130		I			I	L		N	I	Y	L	L	V	Р	P		14
131		F			L	A	N	I	Y	L	L	V	P	P	V		. 14
]			L	V	P	P	v	L	N	P	I	v			
132		7				L			I	v	Y	G	v		Т		
133	3 284	'	, r	Ľ	٧	יי	-1	-	_	•	-	_	٠		43		
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HLA-DRB1*0401 (DR4Dw4) 15-mers (SEQ ID NOS 2672-2805, respectively in order of appearance)

Pos 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 8 core 134 302 Q R I L R L F H V A T H A S E 14

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	145	ĸ	I	G	v	Α	A	V	V	R	G	Α	Α	ь	М	Α	28
2	122	F	D	R	Y	V	Α	1	С	н	P	L	R	Н	A	Т	25
3	217	s	F	s	Y	L	L	Ι	L	ĸ	Т	V	L	G	L	\mathbf{T}	25
4	197	N	V	V	Y	G	L	Ι	V	I	Ι	s	А	1	G	\mathbf{L}	24
5	10	s	Α	Т	Y	F	I	L	Ι	G	\mathbf{L}	Ρ	G	L	E	E	23
6	255	P	F	I	G	L	s	M	V	H	R	F	S	K	R	R	23
7	44	И	L	T	I	1	Y	I	V	R	T	Ε	Н	S	L	Н	22
8	59	E	Р	М	Y	Ι	F	Γ	C	M	\mathbf{L}	S	G	Ι	D	Ι	22
9	158	M	A	Р	L	Р	V	F	Ι	K	Q	\mathbf{L}	Р	F	C	R	22
10	237	K	A	F	G	T	C	V	S	н	V	С	A	V	F	I	22
11	74	L	I	S	T	S	S	M	Ρ	K	М	L	A	Ι	F	W	21
12	134	H	A	\mathbf{T}	V	L	Т	L	Р	R	V	Т	K	I	G	V	20
13	137	v	L	T	L	P	R	V	Т	K	Ι	G	V	A	A	V	20
14	162	P	V	F	I	K	Q	L	P	F	С	R	S	N	I	L	20
15	199	V	Y	G	L	1	V	I	Ι	S	A	I	G	L	D	S	20
16	224	L	K	Т	٧	L	G	L	Т	R	E	A	Q	A	K	A	20
17	256	F	1	G	L	S	M	V	H	R	F	S	K	R	R	D	20
18	290	P	Ī	V	Y	G	V.	K	T	K	Е	Ι	R	Q	R	Ι	20
19	301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	20
20	65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	19
21	100	L	L	Q	I	F	A	Ι	H	S	L	S	G	M	E	S	19
22	196	V	И	V	٧	Y	G	L	I	V	I	Ι	S	A	I	G	19
23 24	218 247	F	S A	Y	L F	L	I F	T T	K V	T P	V F	L	G	L L	T	R	19
24	247	P	V	V	r L	A	N	I	v Y	L	L	A T	G P	Ъ	s V	M L	19 19
26	45	L	T	I	I	Y	I	Λ	R	Т	E	Н	S	L	v Н	E	19
27	68	L	S	G	I	D	I	L	I	s	T	S	S	М	P	K	18
28	80	M	P	K	м	ь	A	I	F	W	F	N	s	Т	T	I	18
29	97	D	A	C	L	L	Q	I	F	A	I	Н	s	L	s	G	18
30	103	I	F	A	I	Н	s	L	s	G	M	E	S	T	v	L	18
31	208	A	I	G	L	D	s	L	L	I	s	F	s	Y	L	L	18
32	249	V	F	I	F	Y	v	P	F	I	G	L	s	М	v	Н	18
33	61	М	Y	I	F	L	С	М	L	s	G	Ι	D	I	L	I	17
34	215	L	I	s	F	s	Y	L	L	I	L	K	Т	V	L	G	17
35	259	L	s	М	v	Н	R	F	s	ĸ	R	R	D	S	P	L	17
36	278	A	N	Ι	Y	L	L	V	P	P	V	L	N	P	Ι	v	17
37	288	L	N	P	I	V	Y	G	V	K	\mathbf{T}	K	E	I	R	Q	17
38	11	A	Т	Y	F	I	L	1	G	L	р	G	L	E	E	A	16
39	24	E	Α	Q	F	W	L	A	F	P	L	С	s	L	Y	L	16
40	42	L	G	N	L	\mathbf{T}	I	I	Y	I	V	R	Т	E	H	S	16
41	253	Y	V	P	F	1	G	L	S	M	٧	Н	R	F	S	K	16
42	47	I	Ι	Y	I	V	R	T	Ε	H	S	L	Н	E	P	М	15
														2	14		

HLA-DRB1*1101 15-mers (SEQ ID NOS 2806-2866, respectively in order of appearance)

	Pos	_	_	_		_	_		0	9	0	1	2	3	4	5	score
		1	2	3	4	5	6	7	8	_	-		_	-	-	_	1.5
43	99	C	L	L	Q	1	F	A	Ι	H	S	L	S	G	M	E	15
44	116	v	L	L	Α	М	A	F	D	R	Y	V	А	Ι	C	Η	15
45	143	V	\mathbf{T}	K	I	G	v	Α	Α	V	V	R	G	Α	Α	L	15
46	179	S	Y	С	L	Н	Q	D	V	M	K	\mathbf{L}	A	С	D	D	1.5
47	227	v	L	G	L	\mathbf{T}	R	E	Α	Q	A	K	А	F	G	Т	15
48	260	s	М	V	H	R	F	S	K	R	R	D	S	P	L	P	15
49	261	M	v	Н	R	F	s	K	R	R	D	S	P	L	P	V	15
50	277	L	Α	N	I	Y	L	L	V	P	Р	v	L	И	P	Ι	15
51	285	P	P	V	L	N	P	I	V	Y	G	V	K	Т	K	E	15
52	114	s	Т	V	L	L	Α	М	Α	F	D	R	Y	V	Α	I	14
53	125	Y	V	Α	I	С	н	Ρ	L	R	Н	Α	Т	V	L	Т	14
54	126	v	Α	I	C	H	P	L	R	н	Α	\mathbf{T}	V	L	T	L	14
55	140	L	P	R	v	\mathbf{T}	ĸ	Ι	G	V	Α	Α	V	V	R	G	14
56	170	F	C	R	S	N	I	L	S	H	S	Y	C	L	Н	Q	14
57	180	Y	C	L	н	Q	D	V	Μ	K	L	Α	C	D	D	I	14
58	193	D	I	R	v	N	v	V	Y	G	L	Ι	V	I	I	S	14
59	229	G	L	Т	R	E	A	Q	Α	K	Α	F	G	\mathbf{T}	C	V	14
60	270	D	s	Р	L	P	v	I	L	A	N	I	Y	L	L	V	14
61	298	ĸ	E	I	R	Q	R	1	L	R	L	F	H	V	A	Т	14

Please replace Table XXIX, beginning at page 213, line 1, with the following rewritten Table XXIX:

-- Table XXIX. Nucleotide sequence in the 5' region close to 101P3A11 gene (SEQ ID NO: 2867).

/).						
,	1 TGCGCTCCA	CAAGCCTGG	C TAACTTTTG	C ATTTTTAATA	A GAGGCAGGG	TTCACCATGT
61	TGGCCTGGCT	GGTCTCGAAC	CCCTGACCTT	GCGATCTGCC	CACCTCGGCC	TCCCAAAGTG
121	CTGGGATTAC	AGGCGTGAGC	CACTGTACCT	GGCGGGGCTT	ATTGTTTTTT	AAAAAGATTT
181	CCAAAACCTT	GCCCTGGCAA	TTCTGATTTT	CTGGGCCTGG	AGCAGGACCT	GGAGGGATGG
241	TGTTGTCAAT	TACTTTAGAT	GTTTCTATCA	GGAAAGTTTG	AGAAATGGTA	TTCAGGCCTA
301						TCTTAAATTA
361	GATTATAGTA			ACTGAGCCTC		CCCAGACCCA
421	CCCTAACCCC		AGAAGAGCTG	GTCAATGTGG	ACCATTCTGA	GCAATCCTGC
481	AAGTCTACTC			CAGTGCCCTG	GGCAGCAACA	TCAGCTCTGA
541	AGATGCAGGA	CTGTGTTACA	TGTTTTATGA	$\tt GTGGGTCTTC$	ACACACTGAG	ATTCATGGGA
601	CAGTAATAGA	ATCTGCTTGT	GCAGCACTGG	GGCCTTGGAG	GGTCAGGGTA	AGGCTCAAGA
661	TGTCCAGGAA	GTTGTATATA	AGGAGAATCA	GAGCAGAGAG	AGACTAGGGT	TCAGAATTAC
721		TAGTCCTGTT	TGTTACTGTC	ACCACTCCAA	TGCCTTTTCC	TCATTAGTCC
721	TTTCTCTCCT			GTTTCTACTT		
841		TTGTATGCAG	AAGCCCCAGC	TCTTGGTCCC	TATCATAGCC	ACTTCAAATG
901			TACTTCCTTT		CCCTGGCCTG	GGGCCTACCA
	TACACTTTTG			TTATGTATGC	CTTGGCCACC	CTGGGTAACC
961				GGCGACTGCA		TACCTCTTCC
1021	10.100.1	TTTCCACTATT	CACCTAGTCC	TCTCCTCTAT	CACCATGCCC	AAGATGGCCA
1081	TGGCCATGCT	TICCACIAII	CAGGAGATCG	AGTTCAACAT	TTGCCTGGCC	CAGATGTTCC
1141	GTCTTTTCCT	MATGGGCAIC	CAGGAGATCG	CTGTCCTGCT	GGCCATGGCT	TTTGACCGCT
1201	TTATCCATGC	TUTGTCAGCC	GIGGAGICAG	CIGICCIGCI		

					GACAGGGTGT	
					CTTCCCACTG	
					CTCCTTCTGT	
					GGTTTATGGA	
1501	TCCTCTCAGT	CATGGGTGTG	GACTCTCTCT	TCATTGGCTT	CTCATATATC	CTCATCCTGT
1561	GGGCTGTTTT	GGAGCTGTCC	TCTCGGAGGG	CAGCACTCAA	GGCTTTCAAC	ACCTGCATCT
1621	CCCACCTCTG	TGCTGTTCTG	GTCTTCTATG	TACCCCTCAT	TGGGCTCTCG	GTGGTGCATA
1681	$\tt GGCTGGGTGG$	TCCCACCTCC	CTCCTCCATG	TGGTTATGGC	TAATACCTAC	TTGCTGCTAC
1741	CACCTGTAGT	CAACCCCCTT	${\tt GTCTATGGAG}$	CCAAGACCAA	AGAGATCTGT	TCAAGGGTCC
1801	TCTGTATGTT	CTCACAAGGT	$\tt GGCAAGTGAG$	ACACCTTAGT	GTCTCGCTTC	TACTACTACT
1861	ACAGAAGATG	GGAATATTAG	${\tt GATCCTATTG}$	AATGCCTTGG	TGATTAAAGT	ATCAAACCTA
1921	TTGTGCTGTC	TTCTTCCAGC	AATTTAAGTA	GATCATGTAT	${\tt TCTGTCTCCA}$	GGAATGTGTC
1981	AGTACTGAAC	${\tt TTATGACCCT}$	${\tt GTCTGGACAT}$	CCTGGAGAAT	${\tt GACTGCACTA}$	GTCCCTCTGC
2041	TATGGTGGTC	TTGCCTTCTC	CTTCTCTCTC	AGCTAGAAAA	TACATCTAGT	TTTGACATGG
2101	GGAGGCTGTA	AAGATCACAC	CTCATGGTTC	ATTCCAGTTT	TGAAGTATGA	TTTTAATGTT
2161	CTTGCCCCCA	TGTGCCCATG	TTGGTGAATT	TGCATGGACT	ATAAACGTTA	TTGCAAATAC
2221	CCTAAAGTGG	TTACCCAGCC	ATAATCAGGG	GTTAATGAAG	GTATTTGGGG	AATAGTAACT
2281	GGAGAGACAG	CAACAAGACA	AGAGGCAGCT	CACATGCAAT	GTTGAAGTTT	CTGTATGCAA
2341	GAGGGTGTGT	TGGCAGATTT	GTGAAATCTG	CCCATTTGCA	TCTGTATGGC	TCTATATGAC
2401	TATTTGTCCA	TAAGGGTGCC	ATGTATTCTG	GTTGTGGGTG	TGAATGTGTG	GGTGTGTTTA
2461	TGTGGACACT	TGCTTTTCAG	TGTGCGTATA	TGTGAGAGAG	AGGGTGCACA	CATGGAATAC
2521	GTACTGGTTG	TGTCCTGGTG	AGTGTGGTAG	CTATGTCCTG	GCACATGTAT	GTTTCATGAG
					TTAGTTGGTA	
					CAGTACCTTT	
					ATGTGAATGT	
					ATCTTTCAGC	
					TTGTGCGGTA	
					CATATTGTTG	
			Latta LATA III	'I"I"I'AA(;(;(`AA	ACTOR CONTRA	A.C.A.D.C.A.D., D.C.A.C.A.C.A.D.
				TTTAAGGCAA		
3001	GTGTATGTGA	CACGAATGGG	GACAGCATCT	GTATTTCTGA	GCATGGATTG	ATGTGTGGTG
3001 3061	GTGTATGTGA TCTGTATGTA	CACGAATGGG TCTTGGAATG	GACAGCATCT GAGGAGGGAG	GTATTTCTGA ATTGAAGAAG	GCATGGATTG TCTGGCTGTG	ATGTGTGGTG AGCAGCAGAA
3001 3061 3121	GTGTATGTGA TCTGTATGTA ATAATTTCCA	CACGAATGGG TCTTGGAATG AAGTTGAGTG	GACAGCATCT GAGGAGGGAG ACATGACTCT	GTATTTCTGA ATTGAAGAAG AAGATGCCCA	GCATGGATTG TCTGGCTGTG GTTTCTCGGC	ATGTGTGGTG AGCAGCAGAA CTGGGGTCAG
3001 3061 3121 3181	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT	GACAGCATCT GAGGAGGGAG ACATGACTCT GTCAGAATGA	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT	ATGTGTGGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT
3001 3061 3121 3181 3241	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC	GACAGCATCT GAGGAGGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT
3001 3061 3121 3181 3241 3301	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCCTA	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCCC
3001 3061 3121 3181 3241 3301 3361	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCCTA TTCCCTTTTT	ATGTGTGGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCCC GGCTTATCTG
3001 3061 3121 3181 3241 3301 3361 3421	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT	CACGAATGGG TCTTGGAATG AAGTTGAGTC AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCCC	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCCTA TTCCCTTTTT AAAATACAAC	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCCC GGCTTATCTG AATTAGCCGG
3001 3061 3121 3181 3241 3301 3361 3421 3481	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTTT AAAATACAAC CTGAGGCAGG	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCCC GGCTTATCTG AATTAGCCGG AGAAACGCTT
3001 3061 3121 3181 3241 3301 3361 3421 3481 3541	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG
3001 3061 3121 3181 3241 3301 3361 3421 3481 3541 3601	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGTGTC	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAAA	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAAA	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT
3001 3061 3121 3181 3241 3301 3361 3421 3481 3541 3601 3661	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC	CACGAATGGG TCTTGGAATG AAGTTGAGTC AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGTGTC CCTCTGGGAA	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAAA	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAAA	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT
3001 3061 3121 3181 3241 3301 3421 3481 3541 3601 3661 3721	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC GCCGCATGGA	CACGAATGGG TCTTGGAATG AAGTTGAGTC AGCTCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGTGTC CCTCTGGGAA AACTCCCTTA	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAA AGCAAGGGTG AGGCAGGAAG	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAAA	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT TGTAGCATTC	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT ACCTCATTAT
3001 3061 3121 3181 3241 3301 3421 3481 3541 3601 3661 3721 3781	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC GCCGCATGGA TCACCTTGTC	CACGAATGGG TCTTGGAATG AAGTTGAGTC AGCTCAGCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGTGTC CCTCTGGGAA AACTCCCTTA TCATGTCTCA	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAA AGCAAGGGTG AGGCAGGAAG CTGTCCTTCC	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAAA	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT TGTAGCATTC TTGTACTCC	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT ACCTCATTAT ATATTGGATG
3001 3061 3121 3181 3241 3301 3421 3481 3541 3661 3721 3781 3841	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC GCCGCATGGA TCACCTTGTC GAAGTAGAAG	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGTGTC CCTCTGGGAA AACTCCCTTA TCATGTCTCA	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAA AGCAAGGGTG AGGCAGGAAG CTGTCCTTCC ATTTTTAAA	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAA GAGGGGAAGC CTGAAAAAAAC ACATGTCTCA GTCTTTGCCA	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT TGTAGCATTC TTGTTACTCC TGTCTAAGTT	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT ACCTCATTAT ATATTGGATG AATGAGGTTA
3001 3061 3121 3181 3241 3301 3421 3481 3541 3601 3661 3721 3781 3841 3901	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC GCCGCATGGA TCACCTTGTC GAAGTAGAAG ATGGAGGCAG ATGGAGGCAG	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGGGAA AACTCCCTTA TCATGTCTCA TCATGTCTCA CAGAGATGGC	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAA AGCAAGGGTG AGGCAGGAAG CTGTCCTTCC ATTTTTAAA TCCAGGGTTC	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAA GAGGGGAAGC CTGAAAAAAAC ACATGTCTCA GTCTTTGCCA TGATAGCAAG	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT TGTAGCATTC TGTAGCATTC TGTTACTCC TGTCTAAGTT TGTCAGGCTG	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT ACCTCATTAT ATATTGGATG AATGAGGTTA CGTGCTCTGTT
3001 3061 3121 3181 3241 3301 3421 3481 3541 3661 3721 3781 3841 3901 3961	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC GCCGCATGGA TCACCTTGTC GAAGTAGAAG ATGGAGGCAG ATGGAGGCAG AGGCACCAGA	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGGGAA AACTCCCTTA TCATGTCTCA TCATGTCTCA CAGAGATGGC AACTGTTGTC	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAA AGCAAGGGTG AGGCAGGAAG CTGTCCTTCC ATTTTTAAA TCCAGGGTTC ACCAGTTAATT	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAA GAGGGAAGC CTGAAAAAAAC ACATGTCTCA GTCTTTGCCA TGATAGCAAG TTGATGTGGT	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT TGTAGCATTC TTGTTACTCC TGTCTAAGTT TGTCAGGCTG CTGAGTTAGA	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT ACCTCATTAT ATATTGGATG AATGAGGTTA CGTGCTCTGTT ATGTGATG AATGAGGTTA
3001 3061 3121 3181 3241 3301 3421 3481 3541 3661 3721 3781 3841 3901 3961 4021	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC GCCGCATGGA TCACCTTGTC GAAGTAGAAG ATGGAGGCAG ATGGAGGCAGA ATGGAGGCAGA TTGCCATGAT	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGGGAA AACTCCCTTA TCATGTCTCA TCATGTCTCA CAGAGATGGC AACTGTTGTC CAGAGATGGC AACTGTTGTC CTGTTGTC CAGAGATGGC AACTGTTTACA	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAA AGCAAGGGTG AGGCAGGAAG CTGTCCTTCC ATTTTTAAA TCCAGGGTTC ACCAGTAATT TAGCTTGATT	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAA GAGGGAAGC CTGAAAAAAC ACATGTCTCA GTCTTTGCCA TGATAGCAAG TTGATGTGGT TAGCGTGTCC	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT TGTAGCATTC TTGTTACTCC TGTCTAAGTT TGTCAGGCTG CTGAGTTAGA TGTCAGGTTAGA TGTGTTTAGA TGTGTTTAGA	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT ACCTCATTAT ATATTGGATG AATGAGGTTA CGTGCTCTGT ATGGTCTGTT ATGTTCATTAT ATGTTGATG ATGGTCTGTT ATGGTCTGAT ATGGTCTGAT ATGTTAAAACT
3001 3061 3121 3181 3241 3301 3421 3481 3541 3661 3721 3781 3841 3901 3961 4021 4081	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC GCCGCATGGA TCACCTTGTC GAAGTAGAAG ATGGAGGCAG ATGGAGGCAGA ATGGAGGCAGA TTGCCATGAT CACAGTTGTG	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGGGAA AACTCCCTTA TCATGTCTCA TCATGTCTCA CAGAGATGGC AACTGTTGTC CAGAGATGGC AACTGTTGTC CTATTTAACA AAACTGATCA	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAA AGCAAGGGTG AGGCAGGAAG CTGTCCTTCC ATTTTTAAA TCCAGGGTTC ACCAGTTATT TAGCTTGATT GTAAAAAATA	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAA GAGGGGAAGC CTGAAAAAAA GACGGGAAGC ACATGTCTCA TGATAGCAAG TTGATGTGGT TAGCGTGTCC AGGGGAGACC	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT TGTAGCATTC TTGTTACTCC TGTCTAAGTT TGTCAGGCTG CTGAGTTAGA TGTCAGGCTG CTGAGTTAGA TGTGTTCTGA AACTAAAAAC	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT ACCTCATTAT ATATTGGATG AATGAGGTTA CGTGCTCTGT ATGGTCTGTT ATGGTCTCTGT ATGGTCTCTGT ATGGTCTGTT ATGGTCTGTT ATGGTCTGTT ATGGTCTGTT ATGGTCTGTT ATGGTCTGTT ATGGTCTGTT ATGTTGTTC
3001 3061 3121 3181 3241 3361 3421 3481 3541 3661 3721 3781 3841 3901 3961 4021 4081 4141	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC GCCGCATGGA TCACCTTGTC GAAGTAGAAG ATGGAGGCAG ATGGAGGCAG ATGCACCAGA TTGCCATGAT CACAGTTGTG CACAGTTGTG TATTTATAGA	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGGGAA AACTCCCTTA TCATGTCTCA TCATGTCTCA CAGAGATGGC AACTGTTGTC CTATTTAACA AAACTGATCA TGTAGTTTT	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAA AGCAAGGGTG AGGCAGGAAG CTGTCCTTCC ATTTTTAAA TCCAGGGTTC ACCAGTAATT TAGCTTGATT GTAAAAAATA ACTTATTCA	ATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAA GAGGGAAGC CTGAAAAAAC ACATGTCTCA GTCTTTGCCA TGATAGCAAG TTGATGTGGT TAGCGTGTCC AGGGGAGCC AAATACGAGG	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT TGTAGCATTC TGTAGCATTC TGTCTAAGTT TGTCAGGCTG CTGAGTTAGA TGTCTGAGTTAGA TGTGTTCTGA AACTAAAAAC TATTTAGTTT	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT ACCTCATTAT ATATTGGATG AATGAGGTTA CGTGCTCTGT ATGGTCTGTT ATGGTCTGTT ATGGTTGTT ATGGTTGTT ATGGTTGTT ATGGTTGTT ATGTTGATC ATGTTTTAAAACT CATGTTGTTC TACATTCAAA
3001 3061 3121 3181 3241 3361 3421 3481 3541 3661 3721 3781 3901 3961 4021 4081 4141 4201	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC GCCGCATGGA TCACCTTGTC GAAGTAGAAG ATGGAGGCAG ATGGAGGCAG ATGCCATGAT CACAGTTGTC CACAGTTGTC TATTTATAGA TTGTTCTCTA	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGTGTC CCTCTGGGAA AACTCCCTTA TCATGTCTCA TCATGTCTCA CAGAGATGGC AACTGTTGTC CTATTTAACA AAACTGATCA TGTAGTTTTT ACTCTCTAAA	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAA AGCAAGGGTG AGCAGGAAG CTGTCCTTCC ATTTTTAAA TCCAGGGTTC ACCAGTAATT TAGCTTGATT TAGCTTGATT GTAAAAATA ACTTATTCA	GTATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAA GAGGGGAAGC CTGAAAAAAC ACATGTCTCA GTCTTTGCCA TGATAGCAAG TTGATGTGGT TAGCGTGTCC AGGGGAGCC AAATACGAGG ACTATTTTG	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTT AAAATACAA CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT TGTAGCATTC TGTCAGGCTG TGTCTAAGTT TGTCAGGCTG CTGAGTTAGA TGTCTAAGTT TGTCAGGCTG AGCTTAAGT TGTCAGGCTG CTGAGTTAGA TGTGTTCTGA AACTAAAAAC TATTTAGTTT CCCTTAAGGG	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT ACCTCATTAT ATATTGGATG AATGAGGTTA CGTGCTCTGT ATGGTCTGTT ATGGTCTGTT ATGGTTGTT ATGGTTGTT ATGTTGATC ATGTTTTAAAACT CATGTTGTTC TACATTCAAA AGAAACCAGA
3001 3061 3121 3181 3241 3361 3421 3481 3541 3661 3721 3781 3901 3961 4021 4081 4141 4201 4261	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC GCCGCATGGA TCACCTTGTC GAAGTAGAAG ATGGAGGCAG ATGGAGGCAGA TTGCCATGAT CACAGTTGTG TATTTATAGA TTGTTCTCTA TGTCATTGGT	CACGAATGGG TCTTGGAATG AAGTTGAGTG AGCTCAGTCT CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGTGTC CCTCTGGGAA AACTCCCTTA TCATGTCTCA TCATGTCTCA CAGAGATGGC AACTGTTGTC CTATTTAACA AAACTGATCA TGTAGTTTTT ACTCTCTAAA CTTACGTGGC	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAA AGCAAGGGTG AGCAGGAAG CTGTCCTTCC ATTTTTAAA TCCAGGGTTC ACCAGTAATT TAGCTTGATT TAGCTTGATT GTAAAAATA ACTTATTCA ATGTTCTCTG TGGTGTTCGG	ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAA GAGGGAAGC CTGAACACA CTGAACACA TGATGCCA TGATAGCAAG TTGATGTGCCA TGATAGCAAG TTGATGTGTCC AGGGGAGCC AAATACGAGG ACTATTTTG GGTGGGGAGG	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT TGTAGCATTC TGTCAGGCTG CTGAGTTACTC TGTCTAAGTT TGTCAGGCTG CTGAGTTAGA TGTGTTCTGA ACTAAAAAC TATTTAGTTT CCCTTAAGGG GTTAAAGAAA	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT ACCTCATTAT ATATTGGATG AATGAGGTTA CGTGCTCTGT ATGGTCTGT ATGGTCTGT ATGGTCTGT ATGGTCTGAT ATTTAAAACT CATGTTGTTC TACATTCAAA AGAAACCAGA CCACGTTCTC
3001 3061 3121 3181 3241 3301 3361 3421 3541 3601 3721 3781 3961 4021 4081 4141 4201 4261 4321	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC GCCGCATGGA TCACCTTGTC GAAGTAGAAG ATGGAGGCAG ATGGAGCAGA TTGCCATGAT CACAGTTGTG TATTTATAGA TTGTTCTCTA TGTCATTGGT TGTCCTCAGC	CACGAATGGG TCTTGGAATG AAGTTGAGTG AAGTTGAGTC CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGTGTC CCTCTGGGAA AACTCCCTTA TCATGTCTCA TCAGAGATGGC AACTGTTGTC CTATTTAACA AAACTGATCA TGTAGTTTTT ACTCTCTAAA CTTACGTGGC CAGAAGTTCA	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAA AGCAAGGGTG AGGCAGGAAG CTGTCCTTCC ATTTTTAAA TCCAGGGTTC ACCAGTAATT TAGCTTGATT TAGCTTGATT GTAAAAATA ACTTATTTCA ATGTTCTCTG TGGTGTTCGG GTAATCCAAG	ATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAA GAGGGGAAGC CTGAAAAAAA GATTTTTGCCA TGATTGTGTT TAGCGTGTCC AGGGGAACC AAATACGAGG ACTATTTTTG GGTGGGGAGG GCCAGAGAGT	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT TGTAGCATTC TGTCAAGCTT GTCTAAGTT TGTCAGGCTG CTGAGTTAGA TGTGTTTCTGA AACTAAAAAC TATTTAGTTT CCCTTAAGGG GTTAAAGAAA GGACGGCAGA	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT ACCTCATTAT ATATTGGATG AATGAGGTTA CGTGCTCTGT ATGGTCTGAT ATGTTTAAAACT CATGTTGTTC TACATTCAAA AGAAACCAGA CCACGTTCTC GGCACTGTCC
3001 3061 3121 3181 3241 3301 3361 3421 3541 3601 3721 3781 3961 4021 4081 4141 4201 4261 4321 4381	GTGTATGTGA TCTGTATGTA ATAATTTCCA CCTGGGTGAT TTTCACAGGC ACCTCTTCCT TCCTGCCTCA CCAAACATGT GTGTGATGGC GAGCCCGCAA ACAGAGCAAG TCTCCTAATC GCCGCATGGA TCACCTTGTC GAAGTAGAAG ATGGAGGCAG ATGGAGCAGA TTGCCATGAT CACAGTTGTG TATTTATAGA TTGTTCTCTA TGTCATTGGT TGTCCTCAGC CTGGGGACCT	CACGAATGGG TCTTGGAATG AAGTTGAGTG AAGTTGAGTC CAGACCACAC ACGTTTCCTG ATAGCAAGTC ATAAAAGTCC GCGTGCCTGT GGTGGAGGTT ACTCTGTGTC CCTCTGGGAA AACTCCCTTA TCATGTCTCA TCAGAGATGGC AACTGTTGTC CTATTTAACA AAACTGATCA TGTAGTTTTT ACTCTCTAAA CTTACGTGGC CAGAAGTTCA TGGTTATAAG	GACAGCATCT GAGGAGGAG ACATGACTCT GTCAGAATGA CTTCTTCATC CCTCTGCTAT ATGGTATCCT TTGGTTCCCC AGTCCCAGCT GCAGTGAGCC AAAAAAAAA AGCAAGGGTG AGGCAGGAAG CTGTCCTTCC ATTTTTAAA TCCAGGGTTC ACCAGTAATT TAGCTTGATT TAGCTTGATT GTAAAAATA ACTTATTTCA ATGTTCTCTG TGGTGTTCGG GTAATCCAAG TTATCCAGAC	ATTTCTGA ATTGAAGAAG AAGATGCCCA AAGGAAACAC CTGAACACAA CCGAGGCACT CACCTCTCCC ATCTTACTA AGTTGGGAGG GAGATCATGC AAAAAAAAA GAGGGGAAGC CTGAACAAAC CTGAACACAC ACATGTCTCA TGATAGCAAG TTGATGTGGT TAGCGTGTCC AGGGGAACC AAATACGAGG ACTATTTTTG GGTGGGGAGG GCCAGAGAGT ACAGGGACCA	GCATGGATTG TCTGGCTGTG GTTTCTCGGC GGTGCTTCCT GGATTTCAAG GGCCTCCTA TTCCCTTTT AAAATACAAC CTGAGGCAGG CACTGCACTC AGCCTTGGTT CAGTCAATCT TGTAGCATTC TGTCAGGCTG CTGAGTTACTC TGTCTAAGTT TGTCAGGCTG CTGAGTTAGA TGTGTTCTGA ACTAAAAAC TATTTAGTTT CCCTTAAGGG GTTAAAGAAA	ATGTGTGTG AGCAGCAGAA CTGGGGTCAG TGCTCCACCT GGCTTTTGTT AACCCTGCCC GGCTTATCTG AATTAGCCGG AGAAACGCTT CAGCCTGGTG GTAGGGAGTT CCCTTCTGTT ACCTCATTAT ATATTGGATG AATGAGGTTA CGTGCTCTGT ATGGTCTGAT ATGTTTAAAACT CATGTTGTTC TACATTCAAA AGAAACCAGA CCACGTTCTC GGCACTGTCC GACAAAAAAA

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4501 GGACCTAAAC AGTGTCCCC AAATGAGAGA AGGGAGGACA GAAAGAACAC TTCAGGATGG
4561 AAATGGGCTG ACACTTAACC GTGGAGTGT TCTGCAAACT TCCTTTGCCA TTCTCCTGTT
4621 TGAGTTTGAT AAACCTGAGA AGAGACTTGG ATAAAGACCG TCACGAAGAC TACACTAATG
4681 AGTTTCTTCT AGCTTTTCT TACTCACTTT CCCTATCTAT CCTTCACATT GGGAGTTGGC
4741 ATGAGGATCC CAGCAGCCA TCAGGGGAGG ACTCTAGAGA TCCCTTTCCC CATTGCCTCT
4801 CCTCCCATA CCCCAGGCA TACCCTCCA GGGCACGGAA GCTGAGAAGC AGTCCAGAAC
4861 CACAGTGGGC TAGTGAGGGG TACCTGCTGA TGTACCCTTT GGACAGCAT CTGCCCCACC
4921 CTGCAGGAAG AAGCAGAAGG AGGGAGAGGG TGAGGAGAG AATAAATAAC CCTGACCAGG
4981 GAGGTCCAAG GGAGTAGGCG GAGACAGGA GGCGGAA GCTGAGAGC TCGCCCACC
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Note: The three high score predictions of promoters were bold and underlined. The lower case sequence indicates the beginning part of the transcript of 101P3A11 gene.--

Please replace Table XXX, beginning at page 214, line 35, with the following rewritten Table XXX:

-- Table XXX: Promoters and their positions predicted by Neural Network Promoter Prediction computer program. (various portions of SEQ ID NO: 2867, respectively, in order of appearance)

Start	End	Score	Promoter Sequence
25	75	0.91	${ t TTTTGCATTTTTAATAGAGGCAGGGTTTCACCATGTTGGCCTGGCTGG$
665	715	0.95	CAGGAAGTTGTATATAAGGAGAATCAGAGCAGAGAGAGACTAGGGTTCAG
2477	2527	0.91	TCAGTGTGCGTATATGTGAGAGAGAGGGTGCACACATGGAATACGTACTG
3139	3189	0.82	TGACATGACTCTAAGATGCCCAGTTTCTCGGCCTGGGGTCAGCCTGGGTG
3420	3470	0.96	GCCAAACATGTATAAAAGTCCTTGGTTCCCCATCTCTACTAAAAATACAA
4092	4142	0.99	AACTGATCAGTAAAAAATAAGGGGAGACCAACTAAAAACCATGTTGTTCT
4953	5003	0.97	AGGCAGAGAATAAATAACCCTGACCAGGGAGGTCCAAGGGAGTAGGCGGA

Please replace Table XXXI, beginning at page 215, line 1, with the following rewritten Table XXXI:

-- Table XXXI: Alignment of five homologous 5' upstream genomic regulatory regions of the human 101P3A11 and PSA genes.

Query: 5' upstream regulatory region of the PSA gene Subject: Putative 5' upstream regulatory region of the 101P3A11 gene.

Nucleic acid sequences predicted to be binding sites for the indicated transcription factors are **bolded**, <u>underlined</u>, or *italicized*.

(SEQ ID NO:	
	gtgattetectgeeteageeteetgagttgetgggattaeaggeatgeageaceatgeee 3983
Query: 3984	agctaatttttgtatttttagtagagatgggg 4015

47

Sbjct: 3478	
(SEQ ID NO:	cctgtaatcccagctactgaggaggctgaggcaggagaatcacttgaacccagaaggcag 4729 2870)
(SEQ ID NO:	2871) SP1 NF-E
	NF-1 NF-1 GR GR aggttgcaatgagccgagattgcgccactgcactccagcctgggtgacagagtgagactc 4789
	tgtctcaaaaaaaaaaa 4807 tgtgtcaaaaaaaaaa 3632
3.	GR NF-1 SP1
Query: 142 (SEQ ID NO:	tgagactgagtctcgctctgtgcccaggctggagtgcagtggtgcaaccttggctcactg 201 2872)
Sbjct: 3621 (SEQ ID NO:	tgacacagagtcttgctctgtcaccaggctggagtgcagtggcatgatctcggctcactg 3562
Query: 202 Sbjct: 3561	caagctccgcctcctgggttcacgccattctcctgcctcagcctcctgagtagctgggac 261
Query: 262 Sbjct: 3501	NF-1 tacaggcacccgccaccacgcctggctaannnnnnngtatttttagtagagatgggg 318
(SEQ ID NO:	
Sbjct: 31 (SEQ ID NO:	SP1 NF-1
	LF-A1 gtgatctgccaccttggcctcccaaagtgctgggattacaggcgtgagccactgcgcct 419
	F-1
Query: 420	ggc 422
Sbjct: 151	

5.

REMARKS

The Specification has been amended to correct erroneous sequence identification numbers and include sequence identification numbers which were omitted at the time of filing.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "<u>Version with markings to show changes made.</u>".

The undersigned hereby states that the compact disc copy of the Sequence Listing and the computer readable form copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.825(a) and (b), respectively, are the same and contain no new matter. Accordingly, entry of the Sequence Listing into the above-captioned case is respectfully requested.

In the unlikely event that the patent office determines that extensions and/or other relief is required, applicant petition for any required relief including extensions of time and authorize the assistant commissioner to charge the cost of such petitions and/or fees due to our deposit account no. <u>03-1952</u> under order no. <u>511582002420</u>. The assistant commissioner is <u>not</u> authorized to charge the cost of the issue fee to the deposit account.

Respectfully submitted,

Dated: May 20, 2002

By:

Kate H. Murashige Registration No. 29,959

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

The paragraph beginning at page 7, line 21, has been amended as follows:

Figure 1. 101P3A11 SSH sequence (SEQ ID NO:2960). The 101P3A11 SSH sequence.

The paragraph beginning at page 7, line 22, has been amended as follows:

Figures 2A-2D. The cDNA (SEQ ID. NO. :2961) and amino acid sequence (SEQ ID. NO. :2962) of 101P3A11. The start methionine is underlined. The open reading frame extends from nucleic acid 133 to 1086 including the stop codon (the codon for the initial M is omitted as the shorter peptide has a more favorable Kozak sequence).

The paragraph beginning at page 7, line 26, has been amended as follows:

Figure 3. Amino acid sequence of 101P3A11 (SEQ ID. NO. :piece of 2962). The 101P3A11 protein has 317 amino acids.

The paragraph beginning at page 7, line 28, has been amended as followsh:

Figure 4. Alignment of 101P3A11 (Sbjct) (SEQ ID NO: 2964) with mouse olfactory receptor S25 (Query.) (SEQ ID NO: 2963) The transmembrane regions of 101P3A11 and mouse olfactory receptor S25 (ORS25) predicted using the TMHMM algorithm are highlighted in gray. The amino acids of ORS25 predicted (Floriano, W.B., et al, 2000, Proc. Natl. Acad. Sci., USA, 97:10712-10716) to be involved in binding of the ligand hexanol and/or involved in the formation of the ligand binding pocket are italicized and bolded in the Figure, and are: Leu 131, Val 134, Val 135, Gly 138, Thr139, Ser 193, Ser 197, Phe 225, Ala 230, Ile 231, Gly 234, Thr 284, Phe 287, Gln 300, Lys 302.

The paragraph beginning at page 11, line 31, has been amended as follows:

Figure 23. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2965) with the rat (SEQ ID NO: 2966) GPCR RA1C (gi|3420759). Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%).

The paragraph beginning at page 12, line 1, has been amended as follows:

Figure 24. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2967) with the human prostate specific GPCR (SEQ ID NO: 2968) (gi|13540539). Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%).

The paragraph beginning at page 12, line 3, has been amended as follows:

Figure 25. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2969) with human olfactory receptor 5II12, HOR5 (SEQ ID NO: 2970) (gi|14423836). Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%).

The paragraph beginning at page 36, line 20, has been amended as follows:

Also, different MHC class I molecules prefer a different length of ligands. For example, SYFPEITHI offers predictions for H2-Kb octamers, HLA-A*0201 nonamers and decamers, or HLA-B8 octamers and nonamers. The maximal scores vary between different MHC alleles. Therefore, one can include known ligands/epitopes in order to have an approximation of the scoring. For example, the maximal score for HLA-A*0201 peptides is 36. The well-known epitope GILGFVFTL (SEQ ID NO: 1401) derived from the influenza A matrix protein scores 30. All predicted MHC class II ligands are 15mers, consisting of three N-terminal flanking residues, the nonamer core sequence located within the binding groove, and three C-terminal flanking residues. Thus, anchor residue P1 appears in position 4 of the peptides predicted with "SYFPEITHI".

The paragraph beginning at page 37, line 25, has been amended as follows:

In an embodiment described in the examples that follow, 101P3A11 can be conveniently expressed in cells (such as 293T cells) transfected with a commercially available expression vector such as a CMV-driven expression vector encoding 101P3A11 with a C-terminal 6XHis (SEQ ID NO: 1402) and MYC tag (pcDNA3.1/mycHIS, Invitrogen or Tag5, GenHunter Corporation, Nashville TN). The Tag5 vector provides an IgGK secretion signal that can be used to facilitate the production of a secreted 101P3A11 protein in transfected cells. The secreted HIS-tagged 101P3A11 in the culture media can be purified, e.g., using a nickel column using standard techniques.

The paragraph beginning at page 70, line 3, has been amended as follows:

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in a majority of a genetically diverse population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. Examples of such amino acid bind many HLA Class II molecules include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; [SEQ ID NO: 710] (SEQ ID NO: 1403), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; [SEQ ID NO: 711] (SEQ ID NO: 1404), and *Streptococcus* 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; [SEQ ID NO: 712] (SEQ ID NO: 712) (SEQ ID NO: 1405). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

The paragraph beginning at page 70, line 11, has been amended as follows:

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see*, *e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: aKXVAAWTLKAAa [SEQ ID NO: 713] (SEQ ID NO: 1406), where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either Dalanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

The paragraph beginning at page 80, line 16, has been amended as follows:

Single chain antibodies comprise the variable domains of the heavy and light chain joined by a flexible linker polypeptide, and are expressed as a single polypeptide. Optionally, single chain antibodies are expressed as a single chain variable region fragment joined to the light chain constant region. Well-known intracellular trafficking signals are engineered into recombinant

polynucleotide vectors encoding such single chain antibodies in order to precisely target the intrabody to the desired intracellular compartment. For example, intrabodies targeted to the endoplasmic reticulum (ER) are engineered to incorporate a leader peptide and, optionally, a C-terminal ER retention signal, such as the KDEL (SEQ ID NO: 1407) amino acid motif. Intrabodies intended to exert activity in the nucleus are engineered to include a nuclear localization signal. Lipid moieties are joined to intrabodies in order to tether the intrabody to the cytosolic side of the plasma membrane. Intrabodies can also be targeted to exert function in the cytosol. For example, cytosolic intrabodies are used to sequester factors within the cytosol, thereby preventing them from being transported to their natural cellular destination.

The paragraph beginning at page 86, line 29, has been amended as follows:

pGEX Constructs: To generate recombinant 101P3A11 proteins in bacteria that are fused to the Glutathione S-transferase (GST) protein, all or parts of the 101P3A11 cDNA protein coding sequence are fused to the GST gene by cloning into pGEX-6P-1 or any other GST- fusion vector of the pGEX family (Amersham Pharmacia Biotech, Piscataway, NJ). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with GST fused at the amino-terminus and a six histidine epitope (6X His) (SEQ ID NO: 1402) at the carboxylterminus. The GST and 6X His tags permit purification of the recombinant fusion protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-GST and anti-His antibodies. The 6X His tag (SEQ ID NO: 1402) is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the cloning primer at the 3' end, e.g., of the open reading frame (ORF). A proteolytic cleavage site, such as the PreScission TM recognition site in pGEX-6P-1, can be employed that permits cleavage of the GST tag from 101P3A11-related protein. The ampicillin resistance gene and pBR322 origin permit selection and maintenance of the pGEX plasmids in *E. coli*. In one embodiment, amino acids 86-317 are cloned into the pGEX-2T expression vector, the protein is expressed and purified.

The paragraph beginning at page 87, line 8, has been amended as follows:

pMAL Constructs: To generate, in bacteria, recombinant 101P3A11 proteins that are fused to maltose-binding protein (MBP), all or parts of the 101P3A11 cDNA protein coding sequence are fused to the MBP gene by cloning into the pMAL-c2X and pMAL-p2X vectors

(New England Biolabs, Beverly, MA). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with MBP fused at the amino-terminus and a 6X His (SEQ ID NO: 1402) epitope tag at the carboxyl-terminus. The MBP and 6X His tags (SEQ ID NO: 1402) permit purification of the recombinant protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-MBP and anti-His antibodies. The 6X His (SEQ ID NO: 1402) epitope tag is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the 3' cloning primer. A Factor Xa recognition site permits cleavage of the pMAL tag from 101P3A11. The pMAL-c2X and pMAL-p2X vectors are optimized to express the recombinant protein in the cytoplasm or periplasm respectively. Periplasm expression enhances folding of proteins with disulfide bonds. In one embodiment, amino acids 86-310 is cloned into the pMAL-c2X expression vector, the protein is expressed and purified.

The paragraph beginning at page 87, line 20, has been amended as follows:

pET Constructs: To express 101P3A11 in bacterial cells, all or parts of the 101P3A11 cDNA protein coding sequence are cloned into the pET family of vectors (Novagen, Madison, WI). These vectors allow tightly controlled expression of recombinant 101P3A11 protein in bacteria with and without fusion to proteins that enhance solubility, such as NusA and thioredoxin (Trx), and epitope tags, such as 6X His (SEQ ID NO: 1402) and S-Tag ™ that aid purification and detection of the recombinant protein. For example, constructs are made utilizing pET NusA fusion system 43.1 such that regions of the 101P3A11 protein are expressed as amino-terminal fusions to NusA.

The paragraph beginning at page 88, line 19, has been amended as follows:

pcDNA4/HisMax Constructs: To express 101P3A11 in mammalian cells, the 101P3A11 ORF was cloned into pcDNA4/HisMax Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter and the SP16 translational enhancer. The recombinant protein has XpressTM and six histidine (6X His) (SEQ ID NO: 1402) epitopes fused to the amino-terminus. The pcDNA4/HisMax vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and

simple vector rescue in cell lines expressing the large T antigen. The Zeocin resistance gene allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.

The paragraph beginning at page 88, line 28, has been amended as follows:

pcDNA3.1/MycHis Constructs: To express 101P3A11 in mammalian cells, the 101P3A11 ORF, with a consensus Kozak translation initiation site, was cloned into pcDNA3.1/MycHis Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the myc epitope and 6X His (SEQ ID NO: 1402) epitope fused to the carboxyl-terminus. The pcDNA3.1/MycHis vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability, along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene can be used, as it allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and CoIE1 origin permits selection and maintenance of the plasmid in *E. coli*.

The paragraph beginning at page 89, line 16, has been amended as follows:

PAPtag: The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pAPtag-5 (GenHunter Corp. Nashville, TN). This construct generates an alkaline phosphatase fusion at the carboxyl-terminus of the 101P3A11 proteins while fusing the IgGκ signal sequence to the amino-terminus. Constructs are also generated in which alkaline phosphatase with an amino-terminal IgGκ signal sequence is fused to the amino-terminus of 101P3A11 proteins. The resulting recombinant 101P3A11 proteins are optimized for secretion into the media of transfected mammalian cells and can be used to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter and the recombinant proteins also contain myc and 6X His (SEQ ID NO: 1402) epitopes fused at the carboxyl-terminus that facilitates detection and purification. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the recombinant protein and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

The paragraph beginning at page 89, line 27, has been amended as follows:

ptag5: The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pTag-5. This vector is similar to pAPtag but without the alkaline phosphatase fusion. This construct generated 101P3A11 protein with an amino-terminal IgGκ signal sequence and myc and 6X His (SEQ ID NO: 1402) epitope tags at the carboxyl-terminus that facilitate detection and affinity purification. The resulting recombinant 101P3A11 protein was optimized for secretion into the media of transfected mammalian cells, and was used as immunogen or ligand to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

The paragraph beginning at page 90, line 30, has been amended as follows:

Additional pSRα constructs are made that fuse an epitope tag such as the FLAGTM tag to the carboxyl-terminus of 101P3A11 sequences to allow detection using anti-Flag antibodies. For example, the FLAGTM sequence 5' gat tac aag gat gac gac gat aag 3' (SEQ ID NO: 1408) is added to cloning primer at the 3' end of the ORF. Additional pSRα constructs are made to produce both amino-terminal and carboxyl-terminal GFP and myc/6X His (SEQ ID NO: 1402) fusion proteins of the full-length 101P3A11 proteins.

The paragraph beginning at page 141, line 31, has been amended as follows:

The generation of anti-101P3A11 polyclonal Ab (pAb) using an amino-terminal peptide encoding amino acids 1-14 (MVDPNGNESSATYF; [SEQ ID NO:YY] (SEQ ID NO: 1409) as antigen was reported in our Priority Application. The effect of this antibody on 101P3A11 mediated ERK phosphorylation (Figure 38) and cAMP accumulation (Figure 39) was determined. 293T cells were transfected with control or 101P3A11 cDNA. Cells were allowed to rest overnight, and treated with anti-101P3A11 or control Ab in the presence of 0.5% or 10% FBS. Cells were lysed and analyzed by Western blotting with anti-Phospho-ERK and anti-ERK mAb. Figure 38 shows that expression of 101P3A11 induces ERK phosphorylation in cells treated with 0.5 or 10% FBS. Anti-101P3A11 pAb reduced the phosphorylation of ERK in

293T-101P3A11 cells treated with 0.5% FBS. The ERK overlay demonstrated equal loading, supporting the specificity of this data.

Table XIX, beginning at page 186, has been amended as follows:

Table XIX: Motifs and Post-translational Modifications of 101P3A11

N-glycosylation site

Number of matches: 3

- 7-10 NESS (SEQ ID NO: 1410)
- 44-47 NLTI (SEQ ID NO: 1411)
- 90-93 NSTT (SEQ ID NO: 1412)

cAMP- and cGMP-dependent protein kinase phosphorylation site 268-271 RRDS (SEQ ID NO: 1413)

Protein kinase C phosphorylation site 266-268 SKR

Casein kinase II phosphorylation site

Number of matches: 3

- 56-59 SLHE (SEQ ID NO: 1414)
- 2 69-72 SGID (SEO ID NO: 1415)
- 110-113 SGME (SEQ ID NO: 1416)

N-myristoylation site

Number of matches: 4

- 6-11 GNESSA <u>(SEQ ID NO: 1417)</u> 21-26 GLEEAQ <u>(SEQ ID NO: 1418)</u> 111-116 GMESTV (SEQ ID NO: 1419)
- 240-245 GTCVSH (SEQ ID NO: 1420)

G-protein coupled receptors family 1 signature

112-128 MESTVLLAMAFDRYVAI (SEQ ID NO: 1421)

Table XXI, beginning at page 190, line 1, has been amended as follows:

Table XXI: Nucleotide sequence of the splice variant (SEQ ID NO: 1422)

- 1 CACATTCCTT CCATACGGTT GAGCCTCTAC CTGCCTGGTG CTGGTCACAG TTCAGCTTCT
- 61 TCATGATGGT GGATCCCAAT GGCAATGAAT CCAGTGCTAC ATACTTCATC CTAATAGGCC
- 121 TCCCTGGTTT AGAAGAGGCT CAGTTCTGGT TGGCCTCCCA TTGTGCTCCC TCTANCTATG
- 181 CTGTGCTAGT AATTGACAAT CATCTACATG TGCGGACGAG CACGNCGCNG AGCCCNGTAT
- 241 NATTCTGCNG CTTCAGCATG ACACCCTNCA GTCTCAGCCA AAGNGCATCT CNGTCAATCA
- 301 NACACNTGAG CTGTCGTACG AGTTGCATCA TCCTANGGCA GGATCAATGT GCGGNAGGCN

58

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361TGACGCAGTGCACGTACCATGGCAGCAAGACAGGGCCGGTACAAATGGGGGCGAGNCGGG421GTGAAGATGNACCCTCGGGTCANAGAGTGCCTCTGCGCCAAAACCTCCATCATGNNAACA481GNGTATAACGGCGNAGAATCGGNNANGCGCAAGGCTAAGGAAANNCCCAANNCNGGTACT541TTAACCCNGCAAANGGCANCNAAACGGGNGGGTNANTGAACAAGGAAGGNNTGNAACTGG601GCCAAAACGGGNTGGGCAANNNAAGGACTCATGGGNCCAAGGGACGGNAAAAGGGGNAAN661CGGGGCGAAATGNNAAAAACCGGGNCCCGGGGAANAANGAAGGGGAANANGNGTGAAGGA721CNGGGTTCAAGGGAAAAGNAAAACCANGGGNNAGAAACCNTTCNAANGGCCCGGGNANGA781AAGGAANTNNGNNNGGNGAAAAAATCNAAAAAAAGCNGNGGCNNAAAAANGGGGGGAANN841NAAANACCNNGGNCGNNAAAAAACNNAANGNGGGGGGANTANACACGGAAANNNANGGGC901GNNNAAGGGAAATAANNCGGGAACNAAAGNGCAAACCGNACGGNAGGAACGAAACCCACC961GGAGNCGCNNAACGCCNNCNNANCCCGAGCNGAGGTNG
```

Table XXII, beginning at page 190, line 38, has been amended as follows:

Table XXII: Nucleotide sequence alignment of 101P3A11 with the splice variant.

```
Score = 337 bits (175), Expect = 4e-89
Identities = 215/223 (96%), Gaps = 6/223 (2%)
Strand = Plus / Plus
```

Table XXIII, beginning at page 191, line 8, has been amended as follows:

```
Table XXIII: Longest single amino acid sequence alignment of 101P3A11 and the splice variant.

Score = 134 bits (287), Expect(2) = 3e-29

Identities = 51/51 (100%)

Frame = +1 / +3
```

101P3A11: 70 HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 222 (SEQ ID NO: 1425)

HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA

Variant: 3 HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 155 (SEQ ID NO: 1426)

Table XXIV, beginning at page 191, line 16, has been amended as follows:

Table XXIV: Peptide sequences from the translation of the nucleotide sequence of the splice variant .

Open reading	Amino acid sequences
frame	
Frame 1 (SEQ ID	HIPSIRLSLYLPGAGHSSASS*WWIPMAMNPVLHTSS**ASLV*KRLSSGWPPIVLPLXM
NO: 1427)	LC**LTIIYMCGRARRXAXYXSAASA*HPXVSAKXHLXQSXT*AVVRVASSXGRINVRXA
	*RSARTMAARQGRYKWGRXGVKMXPRVXECLCAKTSIMXTXYNGXESXXRKAKEXPXXGT
	LTXQXAXKRXGX*TRKXXNWAKTGWAXXGLMGPRDGKRGXRGEMXKTGXRGXXKGXXXEG
•	XGSREKXNXGXETXXXARXXKEXXXXKKSKKSXGXKXGGXXXPXXXKNXXXGXXTRKXXG
	XXGK*XGNXXANRTXGTKPTGXAXRXXXPEXRX
Frame 2(SEQ ID	TFLPYG*ASTCLVLVTVQLLHDGGSQWQ*IQCYILHPNRPPWFRRGSVLVGLPLCSLXLC
NO: 1428)	CASN*QSSTCADEHXAEPXXILXLQHDTLQSQPKXISVNXTXELSYELHHPXAGSMCGRX
	DAVHVPWQQDRAGTNGGEXG*RXTLGSXSASAPKPPSXXQXITAXNRXXARLRKXPXXVL
	*PXKXXXNGXVXEQGRXXTGPKRXGQXKDSWXQGTXKGXXGAKXXKPGPGEXXRGXXVKD
	XVQGKXKTXGXKPFXXPGXERXXXXXKNXKKAXAXKXGEXKXXGRXKTXXGGXXHGXXXA
	XKGNXXGTKXQTXRXERNPPEXXNAXXXPSXG
Frame 3 <u>(SEQ ID</u>	HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLASHCAPSXYA
NO: 1429)	VLVIDNHLHVRTSTXXSPVXFCXFSMTPXSLSQXASXSIXHXSCRTSCIILXQDQCAXGX
	TQCTYHGSKTGPVQMGAXRGEDXPSGXRVPLRQNLHHXNXV*RRRIGXAQG*GXXQXXYF
'	NPAXGXXTGGXXNKEGXXLGQNGXGXXRTHGXKGRXKGXXGRNXKNRXPGXXEGEXX*RT
	GFKGKXKPXXRNXSXGPGXKGXXXGEKIXKKXXXKXGGXXXTXXXKKXXXGGXXTEXXGR
	XREIXREXKXKPXGRNETHRXRXTPXXXRAEV

Note: Frame 3 gives the longest subsequence that is identical with 101P3A11 amino acid sequence. In this Table each (*)indicates the product of a single stop codon, and 'X' indicates a single unknown amino acid.

Table XXVI, beginning at page 193, line 1, has been amended as follows:

Table XXVI:

HLA Class I Nonamers (SEQ ID NOS 1430-1462, respectively in order of appearance)

	HLA-A1	no	one	ome	ers	3					
	Pos	1	2	3	4	5	6	7	8	9	score
1	245	Н	\underline{v}	C	Α	V	F	I	F	Y	24
2	29	L	A	F	P	L	C	S	L	Y	21
3	41	V	$\overline{\Gamma}$	G	N	L	Т	Ī	Ι	Y	21
4	285	P	P	v	L	N	P	Ī	v	Y	20
5	111	G	M	E	S	Т	v	Ŀ	L	A	19
6	117	L	$\overline{\Gamma}$	A	M	Α	F	D	R	Y	19
7	172	R	\underline{s}	N	Ι	L	s	H	S	Y	19
8	192	D	$\underline{\mathtt{D}}$	I	R	V	N	\underline{V}	V	Y	19
9	212	D	\underline{s}	L	L	I	s	F	s	Y	19
10	57	L	H	E	P	M	Y	I	F	L	18
11	22	L	$\underline{\mathbf{E}}$	E	Α	Q	F	W	L	A	17
12	٠ 9	S	S	A	T	Y	F	I	L	I	16
13	52	R	$\underline{\mathbf{T}}$	E	Н	s	L	H	E	P	16
14	54	E	H	S	L	Н	E	<u>P</u>	M	Y	16
											60

	HLA-A1	no	n	ome	ers	3					
	Pos	1	2	3	4	5	6	7	8	9	score
15	78	S	\underline{s}	M	P	K	M	Ŀ	A	I	16
16	95	Q	$\underline{\mathbf{F}}$	D	Α	C	L	$\underline{\mathbf{L}}$	Q	I	16
17	159	Α	$\underline{\mathbf{P}}$	L	P	V	F	I	K	Q	16
18	183	Н	$\underline{\underline{Q}}$	D	V	M	K	$\overline{\Gamma}$	Α	C	16
19	1	Μ	$\overline{\Lambda}$	D	P	N	G	N	E	S	15
20	5	N	\underline{G}	N	E	S	s	<u>A</u>	Т	Y	15
21	. 210	G	$\underline{\mathtt{L}}$	D	S	L	L	Ī	S	F	15
22	273	L	$\underline{\underline{p}}$	v	I	L	Α	$\overline{\mathbf{N}}$	Ι	Y	15
23	271	S	<u>P</u>	L	P	V	I	$\underline{\mathbf{L}}$	A	N	14
24	91	S	$\underline{\underline{T}}$	T	Ι	Q	F	$\underline{\mathtt{D}}$	A	С	13
25	121	Α	F	D	R	Y	V	A	I	C	13
26	138	L	$\underline{\underline{\mathbf{T}}}$	L	Ρ	R	V	$\underline{\mathbf{T}}$	K	I	13
27	218	F	<u>s</u>	Y	\mathbf{r}	L	Ι	$\bar{\mathbf{r}}$	K	T	13
28	282	L	$\underline{\textbf{L}}$	v	P	P	V	$\overline{\mathbf{L}}$	N	P	13
29	190	A	\underline{C}	D	D	Ι	R	$\overline{\Lambda}$	N	v	12
30	191	С	$\underline{\mathtt{D}}$	D	I	R	٧	$\overline{\mathbf{N}}$	V	v	12
31	. 231	\mathbf{T}	R	E	A	Q	A	K	Α	F	12
32	268	R	$\underline{\mathtt{R}}$	D	S	P	L	$\underline{\mathbf{P}}$	V	I	12
33	270	D	\underline{s}	P	L	P	V	$\underline{\mathtt{I}}$	L	A	12

NOS 1463-1569, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	287	V	L	N	P	I	v	Y	G	v	30
2	14	F	I	L	Ι	G	$_{ m L}$	P	G	L	29
3	28	W	L	Α	F	Р	L	С	s	L	28
4	37	Y	L	Ι	Α	V	L	G	N	L	28
5	222	L	I	L	K	T	V	L	G	L	28
6	66	C	M	L	S	G	Ī	D	Ι	L	26
7	108	s	L	S	G	М	Ē	S	Т	v	26
8	181	C	L	Н	Q	D	\underline{v}	M	K	L	26
9	201	G	L	I	V	Ι	$\underline{\mathtt{I}}$	S	Α	I	26
10	214	L	L	Ι	s	F	<u>s</u>	Y	L	L	26
11	275	V	I	L	Α	N	$\underline{\mathtt{I}}$	Y	L	L	26
12	157	L	M	А	P	L	<u>P</u>	V	F	I	25
13	220	Y	L	L	Ι	L	<u>K</u>	T	V	L	25
14	276	1	L	A	N	I	Y	L	L	v	25
15	279	N	I	Y	L	L	$\overline{\Lambda}$	P	P	v	25
16	138	L	T	L	P	R	$\overline{\Lambda}$	T	K	1	24
17	213	S	L	L	Ι	s	F	S	Y	L	. 24
18	49	Y	I	V	R	T	$\underline{\underline{\mathbf{E}}}$	Н	S	L	23
19	143	V	T	K	Ι	G	\underline{v}	A	Α	v	23
20	188	K	L	Α	С	D	$\underline{\mathtt{D}}$	I	R	v	23
21	198	V	v	Y	G	\mathbf{L}	$\underline{\mathtt{I}}$	V	I	I	23
22	21	G	L	E	E	А	Q	F	W	L	22
23	40	Α	v	\mathbf{L}	G	N	$\overline{\mathbf{L}}$	Т	r	I	22
24	206	I	s	A	Ι	G	$\overline{\Gamma}$	D	s	L	22
25	11	Α	T	Y	F	Ι	$\underline{\underline{\mathbf{r}}}$	Ι	G	L	21
26	60	P	M	Y	I	F	$\underline{\mathtt{L}}$	C	M	Ļ	21
27	135	Α	T	V	\mathbf{L}	T	$\overline{\Gamma}$	P	R	V	21
											61

HLA-A*0201 nonomers(SEQ ID NOS 1463-1569, respectively in order of appearance)

	Pos	1 1	2	4	_	_	7	_	9	score
	1.60	1 2	3		5	6	7	8		0.4
28	160	P L		V	F	Ī	K	Q	L	21
29	174	NI	L	S	Н	<u>s</u>	Y	C	L	21
30	207	S A		G	L	D	S	L	L	21
31	272	PL	P	V	1	Ē	Α	N	I	21
32	283	LV	P	Р	V	$\overline{\mathbf{L}}$	И	P	I	21
33	67	ΜL	S	G	Ι	$\overline{\mathbf{D}}$	I	L	I	20
34	101	ЬQ	Ι	F	Α	Ī	Н	S	L	20
35	282	LL	V	P	P	V	L	N	P	20
36	299	EI	R	Q	R	Ī	L	R	L	20
37	304	I L	R	L	F	H	v	Α	T	20
38	39	ΙA	v	L	G	N	L	Т	I	19
39	45	LT	I	Ι	Y	I	v	R	т	19
40	92	т т	I	Q	F	D	Α	С	L	19
41	110	S G	М	Е	s	T	v	L	L	19
42	127	ΑI	С	Н	Р	Ļ	R	Н	A	19
43	132	LR		Ά	Т	v	L	Т	L	19
44	149	A A		V	R	G	A	A	L	19
45	155	A A		М	A	P P	L	Р	v	19
46	156	AL		A	P	L	P	V	F	19
47	203	ΙV		I	s	≓ A	I	G	L	19
48	208	AI	G	L	D	≏ S	L	L	I	19
49	216	IS	F	S	Y	٦ ا	L	I	L	
50	219	SY		L	I	_	K	Т	A T	19
51			I	L		<u>L</u>				; 19
52	221 223	LL			K	T	V	L	G	19
53	17	I G		T P	V G	<u>L</u>	G	L	T	19
54	33	LC		L	Y	<u>L</u>	E	E A	A V	18
55	34	C S	L	Y	L	$\frac{\mathbf{L}}{\mathbf{I}}$	A	V	L	18 18
56	38	LI	A	v	L	Ġ	N	ь Г	Т	18
57	43	GN		Т	I	I	Y	I	v	18
58	85	AI	F	M	F	N	S	Т	T	18
59	118	LA	М	A	F	D	R	Y	v	18
60	194	IR	V	N	v	v	Y	G	L	18
61	210	G L	D	S	L	Ļ	I	s	F	18
62	215	LI	S	F	S	Y	L	L	I	18
63	246	v c	A	V	F	Ī	F	Y	v	18
64	254	V P	F	I	G	L	s	М	v	18
65	15	I L	I	G	L	= P	G	L	E	17
66	63	I F	L	C	M	- L	S	G	I	17
67	72	D I	L	I	s	T	s	s	M	17
68	93	TI	Q	F	D	Ā	C	L	L	17
69	98	A C	L	L	Q	ĭ	F	A	ī	17
70	111	G M		s	T	v	L	L	A	17
71	120	M A	F	D	R	Y	v	A	I	17
72	167	QL	- P	F	C	Ē.	s	N	I	17
73	197	N V		Y	G	L	I	v	I	17
74	226	ΤV		G	L	T	R	E	A	17
75	281	Y L	L	v	P	- P	V	L	N	17
76	31	F P	L	C	s	L	Y	L	I	16
						_				62
										~~

HLA-A*0201 nonomers (SEQ ID NOS 1463-1569, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
77	56	s	L	Н	E	P	М	Y	I	F	16
78	70	G	I	D	I	L	I	s	Т	s	16
79	78	s	s	М	P	K	M	L	Α	I	16
80	79	s	M	P	K	M	L	Α	Ι	F	16
81	104	F	Α	1	Н	S	L	S	G	M	16
82	119	Α	M	Α	F	D	R	Y	V	Α	16
83	144	Т	ĸ	I	G	V	A	Α	V	v	16
84	147	G	v	Α	Α	V	V	R	G	A	16
85	186	V	M	K	L	A	\underline{C}	D	D	I	16
86	230	L	T	R	E	Α	Q	Α	K	A	16
87	238	Α	F	G	Т	С	$\underline{\underline{v}}$	S	Н	v	16
88	249	V	F	Ι	F	Y	\underline{v}	P	F	I	16
89	302	Q	R	Ι	L	R	Ē	F	Н	v	16
90	303	R	I	L	R	L	F	Н	V	A	16
91	18	G	L	P	G	L	$\underline{\mathbf{E}}$	E	A	Q	15
92	35	S	L	Y	L	Ι	<u>A</u>	V	L	G	15
93	42	L	G	N	L	\mathbf{T}	Ī	Ι	Y	I	15
94	46	\mathbf{T}	I	Ι	Y	Ι	\underline{v}	R	T	E	15
95	69	S	G	I	D	I	Ŀ	Ι	s	T	15
96	76	S	T	S	S	М	$\underline{\mathbf{P}}$	K	M	L	15
97	131	P	L	R	Н	Α	$\underline{\mathbf{T}}$	V	L	T	15
98	137	V	L	Т	L	Р	Ŗ	V	Т	K	15
99	153	R	G	Α	Α	L	M	Α	P	L	15
100	190	Α	С	D	D	I	\underline{R}	V	N	v	15
101	191	С	D	D	I	R	V	N	V	v	15
102	204	V	I	I	s	Α	Ī	G	\mathbf{L}	D	1.5
103	241	Т	C	V	S	Н	V	C	Α	v	15
104	251	I	F	Y	V	P	F	I	G	L	15
105	269	R	D	S	P	L	P	V	I	L	15
106	280	I	Y	L	L	V	P	P	V	L	15
107	306	R	L	F	Н	V	A	T	Н	A	15

NOS 1570-1594, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	148	V	A	A	V	V	R	$\underline{\mathbf{G}}$	Α	A	14
2	119	Α	M	A	F	D	R	Y	V	A	13
3	147	G	V	A	A	V	V	R	G	A	12
4	97	D	$\underline{\underline{\mathbf{A}}}$	C	\mathbf{L}	L	Q	<u>I</u>	F	A	11
5	127	Α	Ī	C	Н	P	L	R	Н	A	10
6	3	D	P	N	G	N	E	S	S	A	9
7	17	I	$\underline{\mathbf{G}}$	L	Р	G	L	$\underline{\mathbf{E}}$	E	A	9
8	22	L	E	E	Α	Q	F	M	L	A	9
9	32	P	F	C	s	L	Y	$\mathbf{\underline{L}}$	Ι	A	9
10	77	\mathbf{T}	S	s	M	P	K	M	L	A	9
11	90	N	<u>s</u>	T	Т	Ι	Q	F	D	A	9
12	111	G	M	E	s	Т	V	$\overline{\Gamma}$	L	A	9
											63

HLA A*0203 nonomers (SEQ ID NOS 1570-1594, respectively in order of appearance)

	Pos	1	2	2	4	_	_	7	0	۵	score
			2	3	4	5	О	,	0	9	
13	113	Ε	\underline{s}	T	V	L	L	$\underline{\mathbf{A}}$	М	Α	9
14	141	P	R	v	\mathbf{T}	K	I	G	V	A	9
15	142	R	\underline{v}	T	K	Ι	G	\underline{v}	Α	A	9
16	151	V	V	R	G	A	A	Ŀ	М	A	9
17	182	L	$\overline{\mathbf{H}}$	Q	D	V	M	K	L	A	9
18	200	Y	G	L	I	V	I	I	S	A	9
19	226	\mathbf{T}	V	L	G	L	Т	R	E	A	9
20	228	L	G	L	Т	R	E	A	Q	A	9
21	230	L	$\underline{\mathtt{T}}$	R	E	A	Q	A	K	A	9
22	240	G	$\underline{\mathbf{T}}$	С	V	S	Н	\underline{v}	С	A	9
23	270	D	\underline{s}	P	L	Р	V	<u>1</u>	L	A	9
24	303	R	Ī	L	R	\mathbf{L}	F	$\overline{\mathbf{H}}$	V	A	9
25	306	R	L	F	Н	V	Α	$\underline{\mathtt{T}}$	H	A	. 9

HLA-A26 nonomers (SEQ ID NOS 1595-1675, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	R	0	R	I	L	R	L	30
2	72	D	T	L	T	S	Т	s	s	М	27
3	248	A	v	F	I	F	Y	v	P	F	27
4	210	G	L	D	s	L	Ĺ	I	s	F	26
5	14	F	ī	L	I	G	L	P	G	L	24
6	56	S	L	Н	E	P	М	Y	I	F	24
7	117	L	L	A	М	A	F	D	R	Y	24
8	222	L	I	L	K	Т	v	L	G	L	24
9	245	Н	v	С	Α	v	F	I	F	Y	24
10	11	Α	Т	Y	F	I	L	I	G	L	23
11	37	Y	L	Ι	Α	V	L	G	N	L	23
12	114	s	Т	V	L	L	Α	M	Α	F	23
13	156	Α	L	M	Α	P	L	Р	V	F	23
14	162	P	V	F	I	K	Q	L	P	F	23
15	181	С	L	Н	Q	D	v	M	ĸ	L	23
16	28	W	L	Α	F	P	L	С	S	L	22
17	92	Т	T	Ι	Q	F	D	Α	С	L	22
18	160	P	L	P	V	F	I	K	Q	L	22
19	203	I	V	Ι	1	S	Α	Ι	G	L	22
20	213	s	L	L	Ι	S	F	S	Y	L	22
21	275	V	Ι	L	Α	N	I	Y	L	L	22
22	193	D	Ι	R	V	N	V	V	Y	G	21
23	242	C	V	S	Н	V	C	A	V	F	21
24	76	S	T	S	S	M	P	K	M	L	20
25	253	Y	V	P	F	Ι	G	L	S	M	20
26	274	P	V	Ι	L	A	N	Ι	Y	L	20
27	23	E	E	A	Q	F	W	L	Α	F	19
28	41	V	L	G	N	L	\mathbf{T}	I	I	Y	19
29	49	Y	Ι	V	R	T	E	Н	S	L	19
30	150	Α	V	V	R	G	A	A	L	M	19
										f	64

HLA-A26 nonomers (SEQ ID NOS 1595-1675, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
31	174	N	I	L	S	Н	s	Y	C	L	19
32	192	D	D	I	R	v	И	v	v	Y	19
33	214	L	L	I	s	F	s	Y	L	L	19
34	251	I	F	Y	V	P	F	I	G	L	19
35	231	E	S	s	A	Т	Y	F	I	L	18
36	21	G	L	E	E	A	Q	F	M	L	18
37	45	L	Т	I	I	Y	I	v	R	Т	
38	54	E	Н	S	L		E		M		18
39	59	E	n P	M	У	H	F	P		Y	18
						T		L	C	M	18
40	88	W	F	N	S		T	I	Q	F	18
41	93	T	Ι	Q	F	D	A	C	L	Г	18
42	185	D	V	M	K	L	A -	C	D	D	18
43	198	V	V	Y	G	L	Ι	V	I	I	18
44	62	Y	1	F	Ļ	C	M	L	S	G	17
45	70	G	Ι	D	Ι	L	I	S	T	S	17
46	79	S	M	Ρ	K	M	L	Α	Ι	F	17
47	96	F	D	A	С	L	L	Q	Ι	F	17
48	104	F	A	Ι	Н	S	L	S	G	M	17
49	138	L	Т	L	P	R	V	T	K	Ι	17
50	143	. v	Т	K	Ι	G	V	A	A	V	17
51	204	V	I	Ι	S	A	Ι	G	L	D	17
52	212	D	S	L	L	Ι	S	F	S	Y	17
53	220	Y	L	L	1	L	K	Т	V	L	17
54	256	F	1	G	L	S	M	V	Н	R	17
55	283	L	V	Ρ	Ρ	V	L	N	P	I	17
56	29	L	Α	F	Ρ	L	С	S	L	Y	16
57	40	Α	V	L	G	N	L	Т	Ι	Ι	16
58	46	Т	Ι	Ι	Y	Ι	V	R	Т	Е	16
59	52	R	Т	Ε	Н	S	L	H	E	P	16
60	75	I	S	T	S	S	M	P	K	M	16
61	91	S	Т	Т	Ι	Q	F	D	A	C	16
62	135	A	Т	V	L	T	L	Ρ	R	V	16
63	147	G	V	A	A	V	V	R	G	Α	16
64	201	G	L	Ι	V	Ι	Ι	s	A	Ι	16
65	257	I	G	L	S	M	V	Н	R	F	16
66	279	И	Ι	Y	L	L	V	P	Ρ	V	16
67	30	Α	F	P	\mathbf{L}	С	S	L	Y	L	15
68	101	L	Q	I	F	A	1	Н	S	L	15
69	115	T	V	L	L	A	M	Α	F	D	15
70	127	Α	Ι	C	Н	P	L	R	Н	Α	15
71	153	R	G	A	Α	L	M	Α	P	\mathbf{L}	15
72	163	V	F	1	K	Q	L	Ρ	F	C	15
73	215	L	Ι	S	F	S	Y	L	\mathbf{L}	I	15
74	216	I	s	F	s	Y	L	L	Ι	L	15
75	225	K	T	V	L	G	L	Т	R	Ε	15
76	272	P	L	Р	V	I	L	Α	N	Ι	15
77	282	L	L	V	P	P	V	L	N	P	15
78	286	P	V	L	N	P	I	V	Y	G	15
79	287	v	L	N	P	Ι	v	Y	G	V	15
											65

HLA-A26 nonomers (SEQ ID NOS 1595-1675, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
80	296	K	Т	K	E	I	R	Q	R	1	15
81	303	R	Т	Τ.	R	T.	F	Н	V	Α	15

HLA-A3 nonomers (SEQ ID NOS 1676-1747, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	137	v	L	Т	L	P	R	v	Т	ĸ	30
2	229	G	L	T T	R	E	A	Q	A	ĸ	27
3	145	K	I	G	v	A	A	× V	v	R	26
4	150	A	v	× V	R	G	A	Ă	L	M	24
5	290	P	I	v	Y	G	v	K	Т	ĸ	24
6	35	S	L	· Y	L	I	Ā	v	L	G	23
7	156	A	L	M	A	P	L	P	v	F	23
8	47	I	I	_ Y	I	v	R	_ T	Е	н	22
9	50	r	v	R	т	Е	H	s	L	н	22
10	142	R	v	$^-$	к	I	G	v	Α	Α	22
11	151	v	v	R	G	Α	Ā	L	М	Α	22
12	242	С	v	s	Н	V	C	A	v	F	22
13	248	Α	v	F	1	F	Y	v	Р	F	22
14	116	V	L	L	Α	M	A	F	D	R	21
15	192	D	D	I	R	v	N	v	v	Y	21
16	303	R	I	L	R	L	F	H	v	Α	21
17	304	I	L	R	L	F	Н	v	Α	т	21
18	108	S	L	s	G	M	E	s	Т	v	20
19	198	V	v	Y	G	L	I	v	I	I	20
20	291	I	v	Y	G	v	K	T	K	E	20
21	15	I	L	I	G	L	P	G	L	E	19
22	44	N	L	T	Ι	1	Y	I	V	R	19
23	73	I	L	I	s	Т	s	s	М	P	19
24	74	L	I	S	Т	s	s	М	P	ĸ	19
25	99	C	L	Ļ	Q	Ι	F	A	Ι	H	19
26	162	P	V	F	Ι	K	Q	L	₽	F	19
27	203	I	v	I	I	s	A	I	G	L	19
28	221	L	L	Ī	L	K	$\underline{\underline{\mathbf{T}}}$	\underline{v}	L	G	19
29	245	Н	v	$\underline{\mathbf{c}}$	A	V	F	Ī	F	Y	19
30	306	R	L	F	Н	V	A	T	Н	A	19
31	40	Α	v	$\underline{\mathbf{L}}$	G	N	$\underline{\mathbf{L}}$	$\underline{\mathbf{T}}$	1	I	18
32	85	Α	I	$\underline{\mathbf{F}}$	W	F	$\overline{\mathbf{N}}$	<u>s</u>	Т	T	18
33	205	I	I	\underline{s}	A	Ι	$\underline{\mathbf{G}}$	$\underline{\mathtt{L}}$	D	S	18
34	220	Y	L	$\underline{\underline{\Gamma}}$	Ι	L	$\underline{\mathbf{K}}$	$\underline{\underline{T}}$	V	L	18
35	253	Y	V	$\underline{\underline{P}}$	F	Ι	G	$\overline{\mathbf{L}}$	S	M	18
36	37	Y	L	Ī	A	V	$\overline{\Gamma}$	\underline{G}	N	L	17
37	41	V	L	\underline{G}	N	L	$\underline{\underline{T}}$	Ī	Ι	Y	17
38	117	L	L	$\underline{\underline{\mathbf{A}}}$	M	A	$\underline{\mathbf{F}}$	$\underline{\mathtt{D}}$	R	Y	17
39	131	P	L	$\underline{\mathbf{R}}$	H	A	$\underline{{\bf T}}$	$\underline{\mathtt{v}}$	L	T	17
40	136	T	V	$\overline{\mathbf{r}}$	T	L	$\underline{\underline{P}}$	$\underline{\underline{R}}$	V	T	17
41	180	Y	C	$\overline{\mathbf{r}}$	Н	Q	$\overline{\mathbf{D}}$	$\overline{\Lambda}$	M	K	17
											66

HLA-A3 nonomers (SEQ ID NOS 1676-1747, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
42	201	G	L	I	v	I	I	s	A	I	17
43	213	s	L	L	I	S	F	S	Y	L	17
44	256	F	I	G	L	s	M	V	Н	R	17
45	261	M	v	Н	R	F	s	K	R	R	17
46	276	1	L	A	N	I	Y	Ŀ	L	v	17
47	281	Y	L	L	V	P	P	V	L	N	17
48	286	P	v	Ē	N	P	Ī	\underline{v}	Y	G	17
49	288	L	N	<u>P</u>	Ι	V	Y	G	V	K	17
50	309	Н	v	<u>A</u>	\mathbf{T}	Н	A	$\underline{\mathbf{s}}$	Е	P	17
51	1	M	v	$\underline{\mathtt{D}}$	P	N	G	N	Е	S	16
52	56	S	L	$\underline{\mathbf{H}}$	Ε	P	$\underline{\underline{M}}$	Y	Ι	F	16
53	70	G	I	$\underline{\mathtt{D}}$	Ι	L	<u>I</u>	$\underline{\mathbf{s}}$	Т	s	16
54	72	D	I	$\underline{\mathbf{r}}$	Ι	S	$\underline{\underline{\mathbf{T}}}$	$\underline{\underline{s}}$	S	M	16
55	115	Т	v	$\underline{\mathtt{F}}$	L	A	$\underline{\underline{M}}$	<u>A</u>	F	D	16
56	125	Y	v	A	Ι	C	H	P	L	R	16
57	144	T	K	Ī	G	V	$\underline{\underline{\mathbf{A}}}$	$\underline{\underline{A}}$	V	v	16
58	167	Q	L	$\underline{\mathtt{P}}$	F	С	\underline{R}	$\underline{\underline{s}}$	N	I	16
59	175	1	L	\underline{s}	Н	S	Y	$\underline{\underline{C}}$	L	Н	16
60	195	R	v	\overline{N}	V	V	Y	G	L	I	16
61	197	N	V	$\overline{\Lambda}$	Y	G	Ŀ	$\underline{\mathtt{I}}$	V	I	16
62	210	G	L	$\overline{\mathtt{D}}$	S	L	$\underline{\underline{\mathbf{r}}}$	$\underline{\mathtt{I}}$	S	F	16
63	282	L	L	$\overline{\Lambda}$	Ρ	Ρ	$\overline{\Lambda}$	$\overline{\Gamma}$	N	P	16
64	299	E	I	\underline{R}	Q	R	Ī	$\overline{\mathbf{r}}$	R	L	16
65	301	R	Q	\underline{R}	Ι	L	R	$\overline{\Gamma}$	F	Н	16
66	16	\mathbf{L}	I	G	L	P	$\underline{\mathbf{G}}$	$\overline{\mathbf{r}}$	E	E	15
67	46	Т	I	Ī	Y	Ι	V	\underline{R}	Т	E	15
68	102	Q	I	$\underline{\mathbf{F}}$	A	Ι	H	\underline{s}	L	s	15
69	193	D	I	R	V	N	$\overline{\Lambda}$	$\overline{\Lambda}$	Y	G	15
70	208	Α	I	\underline{G}	L	D	<u>s</u>	$\overline{\Gamma}$	L	I	15
71	223	Ι	L	$\underline{\mathbf{K}}$	Т	V	$\underline{\mathbf{L}}$	$\underline{\mathbf{G}}$	L	Т	15
72	237	K	A	$\underline{\mathbf{F}}$	G	Т	\underline{C}	$\overline{\Lambda}$	S	H	15

HLA-B*0702 nonomers (SEQ ID NOS 1748-1812, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	130	Н	P	L	R	Н	Α	Т	v	L	22
2	59	E	P	M	Y	I	F	\mathbf{L}	С	M	21
3	168	L	P	F	С	R	S	N	I	L	20
4	289	N	P	Ι	V	Y	G	V	K	T	19
5	3	D	P	N	G	N	E	S	S	A	18
6	19	L	P	G	L	Ε	E	Α	Q	F	18
7	140	L	P	R	v	Т	K	I	G	v	18
8	284	V	P	P	V	L	N	P	Ι	v	17
9	31	F	P	\mathbf{L}	C	s	L	Y	L	I	16
10	254	V	P	F	Ι	G	L	S	M	v	16
11	269	R	D	S	P	L	P	V	Ι	L	16
12	149	Α	A	V	V	R	G	Α	Α	L	15
											67

HLA-B*0702 nonomers (SEQ ID NOS 1748-1812, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
13	153	R	G	A	A	L	М	A	P	L	15
14	156	A	L	М	A	Р	L	P	V	F	15
15	251	I	F	Y	V	P	F	I	G	L	15
	299	E						L		L	
16 17		E	I S	R S	Q A	R	I	F	R	L	15
	8					T	Y		Ι		14
18	28 30	W	L	A P	F L	P	L S	C L	S	L	14
19		A	F			С			Y	L	14
20	110	S	G	M	E	S	T	V	L	L	14
21	132	L	R	H	A	T	V	L	T	L	14
22	159	A	P	L	P	V	F	I	K	Q	14
23	222	L	I	L	K	Т	V	L	G	L	14
24	271	S	P	L	P	V	I	L	A	N	14
25	25	A	Q	F	W	L	A	F	P	L	13
26	109	L	S	G	M	E	S	Т	V	L	13
27	124	R	Y	V	A	Ι	C	H	P	L	13
28	216	I	S	F	S	Y	L	L	Ι	L	13
29	268	R	R	D	S	P	L	Р	V	I	13
30	280	I	Y	L	L	V	P	P	V	L	13
31	11	A	T	Y	F	Ι	L	Ι	G	Ь	12
32	34	С	s	L	Y	L	Ι	A	V	L	12
33	57	L	H	E	P	M	Y	I	F	r	12
34	76	s	T	S	S	M	P	K	M	L	12
35	142	R	V	Т	K	Ι	G	V	A	A	12
36	151	V	V	R	G	A	A	L	M	A	12
37	190	Α	C	D	D	Ι	R	V	N	V	12
38	194	I	R	V	N	V	V	Y	G	L	12
39	206	Ι	S	A	Ι	G	L	D	S	L	12
40	207	S	A	Ι	G	L	D	S	L	L	12
41	220	Y	L	L	Ι	L	K	Т	V	L	12
42	267	K	R	R	D	S	Р	L	P	v	12
43	304	I	L	R	L	F	Н	V	A	T	12
44	14	F	I	L	Ι	G	L	P	G	L	11
45	23	E	E	A	Q	F	W	L	A	F	11
46	37	Y	L	Ι	A	V	L	G	N	L	11
47	40	A	V	L	G	N	L	Т	Ι	I	11
48	77	Т	s	S	M	P	K	M	L	A	11
49	78	s	s -	M	P	K	M	L	A	I	11
50	80	М	P	K	M	L	A	Ι	F	W	11
51	92	Т	T	Ι	Q	F	D	A	C	L	11
52	112	M	E	S	Т	V	Ь	L	A	M	11
53	119	A	M	Α	F	D	R	Y	V	A	11
54	127	A	I	C	Н	P	L	R	Η	A	11
55	131	P	L	R	Н	A	Т	V	L	Т	11
56	155	A	A	L	M	A	P	L	P	v -	11
57 	157	L	M	A	P	L	P	V	F	I	11
58	181	С	L	H	Q	D	V	M	K	L	11
59	203	I	V	I	Ι	S	A	1	G	L	11
60	208	Α	Ι	G	L	D	S	L	L	Ι	11
61	213	s	L	L	Ι	S	F	S	Y	L	11
											68

HLA-B*0702 nonomers (SEQ ID NOS 1748-1812, respectively in order of appearance)

	Pos			score							
	FUS	1	2	3	4	5	6	7	8	9	SCOLE
62	248	Α	v	F	Ι	F	Y	V	P	F	11
63	265	F	S	K	R	R	D	S	P	L	11
64	275	v	I	L	Α	N	Ι	Y	L	L	11
65	285	Þ	P	v	T.	N	Р	т	V	Y	11

NOS 1813-1847, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	R	Q	R	I	L	R	L	31
2	265	F	s	ĸ	R	R	Ď	s	P	L	29
3	149	A	A	v	v	R	G	A	A	L	24
4	168	L	P	F	C	R	s	N	I	L	24
5	294	G	v	ĸ	Т	ĸ	E	Ι	R	Q	21
6	120	М	Α	F	Đ	R	Y	V	A	I	20
7	292	v	Y	G	V	ĸ	Т	K	Е	I	20
8	21	G	L	E	E	A	Q	F	W	L	19
9	78	s	s	M	p	ĸ	М	L	Α	I	19
10	160	Р	L	P	V	F	I	K	Q	L	19
11	186	V	M	ĸ	L	A	С	D	D	I	18
12	213	S	L	L	I	s	F	S	Y	L	18
13	221	L	L	I	L	K	Т	V	L	G	18
14	296	K	Т	ĸ	E	I	R	Q	R	I	18
15	297	T	K	E	Ι	R	Q	R	I	L	18
16	130	Н	P	L	R	Н	Α	T	V	L	17
17	181	C	L	H	Q	D	V	М	K	L	17
18	223	I	L	K	T	V	L	G	L	T	17
19	28	W	L	A	F	P	L	C	S	L	16
20	37	Y	L	I	A	V	L	G	N	L	16
21	56	S	L	Н	E	P	М	Y	Ι	F	16
22	80	M	Р	K	M	L	A	Ι	F	W	16
23	162	P	V	F	I	K	Q	L	Р	F	16
24	201	G	L	I	V	I	I	S	A	I	16
25	207	S	A	I	G	L	D	S	L	L	16
26	214	L	L	I	S	F	S	Y	L	L	16
27	220	Y	L	L	Ι	L	K	Т	v.	L	16
28	233	E	A	Q	A	K	A	F	G	T	16
29	275	V	Ι	L	A	N	I	Y	L	L	16
30	304	I	L	R	L	F	Н	V	Α	T	16
31	14	F	I	L	I	G	L	P	G	L	15
32	110	S	G	M	E	S	Т	V	L	L	15
33	138	\mathbf{L}	Т	L	P	R	V	T	K	I	15
34	164	F	Ι	K	Q	L	P	F	С	R	15
35	222	L	Ι	L	K	T	V	L	G	L	15

HLA-B*1510 nonomers (SEQ ID NOS 1848-1890, respectively in order of appearance)

Pos										score	
	200	1	2	3	4	5	6	7	8	9	DCCTC
1	57	L	Н	E	P	М	Y	Ι	F	Ł	23
2	244	S	H	V	C	Α	V	F	1	F	17
3	269	R	D	S	Р	L	P	V	I	L	16
4	280	I	Y	L	L	V	P	P	V	L	16
5	262	V	H	R	F	S	K	R	R	D	15
6	299	E	I	R	Q	R	Ι	L	R	L	15
7	106	I	Н	S	$_{\rm L}$	S	G	M	E	S	14
8	206	I	S	Α	Ι	G	\mathbf{L}	·D	S	L	14
9	220	Y	L	L	Ι	L	K	T	V	L	14
10	251	I	F	Y	V	P	F	Ι	G	L	14
11	297	Т	K	Ε	Ι	R	Q	R	Ι	L	14
12	21	G	L	E	E	A	Q	F	W	L	13
13	34	C	s	L	Y	L	I	A	V	L	13
14	54	E	H	S	L	H	E	P	М	Y	13
15	110	S	G	M	E	S	\mathbf{T}	V	L	L	13
16	194	I	R	V	N	V	V	Y	G	L	13
17	8	E	s	S	A	T	Y	F	1	L	12
18	14	F	I	L	I	G	L	P	G	L	12
19	28	W	L	Α	F	P	L	С	S	L	12
20	66	C	M	L	s	G	I	D	Ι	L	12
21	76	S	T	S	S	М	P	K	М	L	12
22	92	Т	T	Ι	Q	F	D	Α	С	L	12
23	109	\mathbf{L}	s	G	M	E	S	T	V	L	12
24	130	Н	P	L	R	Н	Α	T	V	L	12
25	132	L	R	Н	Α	\mathbf{T}	V	L	Т	L	12
26	149	Α	A	V	V	R	G	A	A	L	12
27	153	R	G	A	A	L	M	Α	P	L	12
28	160	P	L	P	V	F	Ι	K	Q	L	12
29	181	C	L	Н	Q	D	V	М	K	L	12
30	182	L	н	Q	D	V	М	K	L	A	12
31	203	1	v	I	I	S	Α	Ι	G	L	12
32	216	I	s	F	s	Y	L	L	Ι	L	12
33	222	L	I	L	K	T	V	L	G	L	12
34	275	V	I	L	A	N	I	Y	L	L	12
35	37	Y	L	Ι	A	V	L	G	N	L	11
36	49	Y	I	V	R	T	E	Н	S	L	11
37	93	T	I	Q	F	D	A	С	L	L	11
38	101	L	Q	1	F	A	Ι	Н	S	L	11
39	129	C	H	P	L	R	Н	Α	Т	v	11
40	133	R	H	A	Т	V	L	\mathbf{T}	L	P	· 11
41	177	S	H	S	Y	С	L	H	Q	D	11
42	207	S	A	Ι	G	L	D	S	L	L	11
43	257	I	G	L	s	M	V	Н	R	F	11

HLA-B*2705 nonomers (SEQ ID NOS 1891-2008, respectively in order of appearance)

•	Pos	1	2	3	4	5	6	7	8	9	score
1	194	I	R	V	N	V	V	Y	G	L	25
2	268	R	R	D	S	P	L	P	V	I	24
3	132	L	R	Н	Α	Т	v	L	\mathbf{T}	L	23
											70

HLA-B*2705 nonomers (SEQ ID NOS 1891-2008, respectively in order of appearance)

-				- <u>F</u>					<u>-</u>		
	Pos	7	2	2	4	_	_	7	0	0	score
4	300	1 I	2 R	3 Q	4 R	5 I	6 L	7 R	8 L	9 F	23
5	305	L	R	L	F	Н	V	A	Т	н	23
6	231	Т	R	E	A	Q	A	K	A	F	21
7	34	C	s	L	Y	L	I	A	V	L	18
8	299	E	I	R	Q	R	I	L	R	L	18
9	2 <i>99</i> 6	G	И	E	s	S	A	Т	Y	F	17
10	66	C	M	L	S	G	I	D	I	L	17
11	162	P	v	F	I	K	Q	L	P	F	17
12	207	s	A	I	G	L	D	S	L		17
13	210	G	L	D	S	L	L		S	L F	17
14	220	Y	L	L	I	L	К	I T	V	L	
15	237	K	A	F	G	Т	C	v	s	н	17
16	269	R	D	S	P	L	P	v	I	L	17
17		I		L	L	V			V		17
	280		Y				P	P		L	17
18	295	V	K	T	K	E	I	R	Q	R	17
19	11	A	T	Y	F	I	L	Ι	G	L	16
20	14	F	I	L	1	G	L	P	G	L	16
21	21	G	L	E	Ε	A	Q	F	W	L	16
22	25	A	Q	F	W	L	A	F	P	L	16
23	37	Y	L	I	A	V	L	G	И	L	16
24	92	. T	T	I	Q	F	D	A	C	L	16
25	101	L	Q	Ι	F	A	I	Н	S	L	16
26	124	R	Y	V	A	Ι	С	Н	Р	L	16
27	130	H	₽	L	R	Н	A	T	V	L	16
28	141	Þ	R	V	Т	K	Ι	G	V	A	16
29	153	R	G	A	A	L	M	A	P	L	16
30	181	С	L	Н	Q	D	V	M	K	L	16
31	201	G	L	Ι	V	Ι	Ι	S	A	Ι	16
32	203	I	V	Ι	Ι	S	A	Ι	G	L	16
33	216	I	S	F	S	Y	L	L	Ι	L	16
34	222	L	I	L	K	T	V	L	G	L	16
35	255	Þ	F	Ι	G	L	S	M	V	Н	16
36	257	Ι	G	Ļ	S	M	V	Н	R	F	16
37	275	V	I	L	A	N	Ι	Y	L	L	16
38	47	I	Ι	Y	I	V	R	Т	Ε	Н	15
39	109	L	S	G	М	E	S	Т	V	L	15
40	114	S	T	V	L	\mathbf{L}	A	M	A	F	15
41	123	D	R	Y	V	A	Ι	C	Η	P	15
42	145	K	I	G	V	A	A	V	V	R	15
43	156	Α		M	A	P	L	Ρ	V	F	15
44	168	L	P	F	C	R	s	N	Ι	L	15
45	172	R	S	N	Ι	L	S	Н	S	Y	15
46	198	V	V	Y	G	L	Ι	V	Ι	I	15
47	206	I	S	A	Ι	G	L	D	S	L	15
48	229	G	L	T	R	E	A	Q	A	K	15
49	248	A	v	F	Ι	F	Y	V	P	F	15
50	251	I	F	Y	V	Р	F	I	G	L	15
51	274	P	v	1	Ļ	A	N	I	Y	L	15
52	290	P	I	V	Y	G	V	K	T	K	15
											71

HLA-B*2705 nonomers(SEQ ID NOS 1891-2008, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
53	298	K	E	I	R	Q	R	I	L	R	15
54	19	L	P	G	L	E	E	Α	Q	F	14
55	29	L	Α	F	P	L	С	s	L	Y	14
56	30	Α	F	P	L	С	s	L	Y	L	14
57	39	1	Α	V	L	G	N	L	Т	I	14
58	40	Α	v	L	G	N	L	Т	I	I	14
59	79	s	M	P	K	М	L	Α	Ι	F	14
60	81	P	ĸ	М	L	Α	Ι	F	W	F	14
61	99	С	L	L	Q	Ι	F	Α	I	н	14
62	137	V	L	T	L	P	R	v	Т	ĸ	14
63	138	$_{ m L}$	T	L	Р	R	v	Т	K	r	14
64	150	Α	v	V	R	G	Α	Α	L	M	14
65	160	P	L	p	V	F	I	K	Q	L	14
66	174	N	I	L	S	Н	s	Y	С	L	14
67	180	Y	С	L	Н	Q	D	V	M	K	14
68	192	D	D	1	R	V	N	V	V	Y	14
69	212	D	s	L	L	I	S	F	s	Y	14
. 70	213	s	L	L	Ι	S	F	S	Y	L	14
71	214	L	L	I	S	F	s	Y	L	L	14
72	260	S	M	V	Н	R	F	s	К	R	14
73	263	Н	R	F	S	K	R	R	D	s	14
74	267	K	R	R	D	s	P	L	Р	v	14
75	293	Y	G	V	K	Т	K	Е	Ι	R	14
76	301	R	Q	R	Ι	L	R	L	F	н	14
77	302	Q	R	Ι	L	R	L	F	Н	v	14
78	5	N	G	N	Ε	S	S	Α	т	Y	13
79	23	E	E	Α	Q	F	W	L	Α	F	13
80	28	W	L	Α	F	P	L	С	S	L	13
81	44	N	L	T	I	I	Y	1	V	R	13
82	51	V	R	Т	E	Η	S	\mathbf{L}	Н	E	13
83	56	S	L	Н	E	P	M	Y	1	F	13
84	60	P	M	Y	Ι	F	L	С	M	L	13
85	72	D	I	L	Ι	S	Т	S	S	M	13
86	74	L	I	S	Т	S	S	M	Ρ	K	13
87	75	I	S	Т	S	S	M	P	K	M	13
. 88	98	Α	С	L	L	Q	Ι	F	A	I	13
89	104	F	A	Ι	Η	S	L	S	G	M	13
90	110	S	G	M	Ε	S	Т	V	L	L	13
91	116	V	L	L	A	M	A	F	D	R	13
92	126	V		Ι	С	Н	P	L	R	H	13
93	149	Α	A	V	V	R	G	A	A	L	13
94	158	М	A	Ρ	L	P	V	F	I	K	13
95	164	F	Ι	K	Q	L	P	F	C	R	13
96	170	F	C	R	S	N	I	L	S	H	13
97	171	С	R	S	N	I	L	S	H	S	13
98	187	M	K	L	A	C	D	D	I	R	13
99	217	S	F	S	Y	L	L	I	L	K	13
100	224	L	ĸ	T	V	L	G	L	Т	R -	13
101	242	С	v	s	Н	V	С	A	V	F	13
											72

NOS 1891-2008, respectively in order of appearance)

	Pos										score
	100	1	2	3	4	5	6	7	8	9	BCOLC
102	256	F	I	G	L	S	М	V	Н	R	13
103	261	M	V	Н	R	F	S	K	R	R	13
104	49	Y	I	V	R	T	E	Н	S	L	12
105	57	L	H	E	P	М	Y	I	F	L	12
106	88	W	F	N	S	Т	\mathbf{T}	Ι	Q	F	12
107	96	F	D	A	С	\mathbf{L}	L	Q	I	F	12
1,08	134	Н	A	Т	V	L	T	L	P	R	12
109	152	V	R	G	Α	Α	L	М	A	P	12
110	179	s	Y	C	L	H	Q	D	V	M	12
111	197	N	v	V	Y	G	L	1	V	I	12
112	244	s	H	V	C	Α	V	F	Ι	F	12
113	265	F	s	K	R	R	D	S	P	L	12
114	273	L	P	V	Ι	L	Α	N	Ι	Y	12
115	285	P	P	V	L	N	P	Ι	V	Y	12
116	288	L	N	P	Ι	V	Y	G	V	ĸ	12
117	296	K	T	K	E	I	R	Q	R	I	12
118	297	Т	ĸ	Е	Ι	R	Q	R	Ι	L	12

HLA-B*2709 nonomers(SEQ ID NOS 2009-2063, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	194	I	R	v	N		v	Y	G	L	24
2	268	R	R	D	S	P	L	P	v	Ι	24
3	132	L	R	Н	Α	T	V	L	Т	L	22
4	267	к	R	R	D	S	P	L	P	V	21
5	300	I	R	Q	R	Ι	L	R	L	F	20
6	231	\mathbf{T}	R	E	Α	Q	Α	K	Α	F	19
7	302	Q	R	Ι	L	R	L	F	Н	V	19
8	124	R	Y	V	A	I	С	Н	P	L	16
9	269	R	D	S	P	L	P	V	I	L	16
10	43	G	N	L	T	I	I	Y	Ι	v	15
11	216	I	S	F	S	Y	L	L	Ι	L	1.5
12	11	Α	T	Y	F	I	L	Ι	G	L	14
13	25	Α	Q	F	M	L	A	F	P	L	14
14	153	R	G	A	А	L	М	Α	P	L	14
15	174	N	Ι	L	S	Н	S	Y	C	L	14
16	222	L	Ι	L	K	Т	V	L	G	L	14
17	257	I	G	L	s	M	V	Н	R	F	14
18	280	Ι	Y	L	L	V	P	P	V	L	14
19	6	G	N	E	S	S	А	Т	Y	F	13
20	14	F	Ι	L	I	G	L	P	G	L	13
21	21	G	L	Ē	E	Α	Q	F	W	L	13
22	66	C	M	L	S	G	I	D	I	L	13
23	130	H	P	L	R	Н	A	T	V	L	13
24	201	G	L	Į	V	I	I	s	Α	I	13
25	203	I	V	I	Ι	s	A	Ι	G	L	13
											73

HLA-B*2709 nonomers(SEQ ID NOS 2009-2063, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
26	214	L	L	Ι	s	F	s	Y	L	L	13
27	251	I	F	Y	V	P	F	Ι	G	\mathbf{L}	13
28	263	Н	R	F	S	K	R	R	D	s	13
29	275	V	I	L	Α	N	Ι	Y	L	L	13
30	305	L	R	L	F	Н	V	Α	T	Н	13
31	30	Α	F	P	L	С	S	L	Y	L	12
32	34	C	S	L	Y	L	Ι	A	V	L	12
33	37	Y	L	Ι	Α	٧	L	G	N	L	12
34	51	V	R	T	E	Н	S	L	Н	Е	12
35	60	P	М	Y	Ι	F	L	C	M	L	12
36	75	I	S	Т	S	s	М	P	K	М	12
37	93	T	Ι	Q	F	D	Α	С	L	L	12
38	123	D	R	Y	V	A	I	С	Н	P	12
39	135	Α	T	V	L	T	L	P	R	V	12
40	138	\mathbf{L}	T	L	P	R	V	T	K	I	12
41	149	Α	Α	V	V	R	G	А	А	\mathbf{L}	12
42	155	Α	Α	L	M	A	P	L	P	V	12
43	168	\mathbf{L}	P	F	С	R	S	N	I	\mathbf{L}	12
44	181	C	L	Н	Q	D	V	М	K	L	12
45	188	K	L	A	C	D	D	Ι	R	V	12
46	190	Α	С	D	D	I	R	V	N	v	12
47	195	R	V	N	V	V	Y	G	L	I	12
48	210	G	L	D	S	L	L	I	S	F	12
49	213	S	L	L	Ι	S	F	S	Y	L	12
50	220	Y	L	L	Ι	L	K	T	V	\mathbf{L}	12
51	248	Α	V	F	I	F	Y	V	Р	F	12
52	279	N	Ι	Y	L	L	V	P	P	V	12
53	287	V	L	N	P	Ι	V	Y	G	V	12
54	296	K	Т	K	E	Ι	R	Q	R	I	12
55	299	E	Ι	R	Q	R	I	L	R	L	12

HLA-B*5101 nonomers (SEQ ID NOS 2064-2132, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	39	I	A	V	L	G	N	L	Т	I	26
2	31	F	P	L	C	S	L	Y	L	I	25
3	120	M	A	F	D	R	Y	V	A	I	24
4	130	Н	P	L	R	Н	Α	Т	V	L	23
5	118	L	A	M	Α	F	D	R	Y	v	22
6	140	L	P	R	V	\mathbf{T}	K	Ι	G	v	22
7	155	Α	A	L	М	A	P	L	Р	v	22
8	42	L	G	N	\mathbf{L}	T	1	Ι	Y	I	21
9	254	V	P	F	I	G	L	S	M	v	21
10	284	v	P	P	V	L	N	P	I	v	21
11	168	L	P	F	C	R	s	N	I	L	20
12	235	Q	A	K	A	F	G	Т	С	v	20
13	138	L	T	L	P	R	V	Т	K	I	19
											7/

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HLA-B*5101 nonomers (SEQ ID NOS 2064-2132, respectively in order of appearance)

•				_	•				_		
	Pos	1	2	3	4	5	6	7	8	9	score
14	159	Α	P	L	P	V	F	I	K	Q	18
15	189	L	Α	С	D	D	Ι	R	٧	N	18
16	198	V	v	Y	G	L	Ι	V	Ι	I	18
17	277	L	A	N	Ι	Y	L	L	V	P	18
18	207	s	A	I	G	L	D	S	L	L	17
19	283	L	v	P	Р	v	L	N	P	I	17
20	63	I	F	L	C	М	L	s	G	I	16
21	86	I	F	W	F	N	s	Т	Т	r	16
22	110	s	G	M	Ε	s	Т	v	L	L	16
23	144	Т	ĸ	I	G	v	Α	Α	V	v	16
24	149	А	A	V	v	R	G	Α	Α	L	16
25	197	N	v	V	Y	G	L	I	V	I	16
26	271	s	P	L	Р	V	I	L	Α	N	16
27	280	I	Y	L	L	٧	P	Р	V	L	16
28	3	D	P	N	G	N	E	s	s	Α	15
29	40	Α	v	L	G	N	L	Т	I	I	15
30	97	D	A	C	L	L	Q	Ι	F	Α	15
31	132	L	R	Н	Α	Т	v	L	Т	L	15
32	222	L	I	L	K	Т	V	L	G	L	15
33	279	N	I	Y	L	L	V	Р	Р	v	15
34	285	P	P	v	L	N	P	Ι	V	Y	15
35	289	N	P	I	V	Y	G	V	K	т	15
36	9	s	s	Α	Т	Y	F	I	L	I	14
37	65	L	С	М	L	s	G	Ι	D	I	14
38	84	L	Α	I	F	W	F	N	s	T	14
39	126	V	Α	I	С	Н	Р	L	R	н	14
40	157	L	М	Α	Р	L	P	V	F	I	14
41	158	M	Α	P	L	p	v	F	Ι	ĸ	14
42	191	С	D	D	Ι	R	V	N	V	v	14
43	200	Y	G	L	I	v	Ι	I	s	Α	14
44	209	I	G	L	D	S	L	L	Ι	s	14
45	215	$_{ m L}$	I	s	F	S	Y	L	L	I	14
46	219	S	Y	L	L	Ι	L	К	Т	v	14
47	220	Y	L	L	Ι	L	K	Т	V	L	14
48	237	К	A	F	G	Т	С	V	s	н	14
49	247	С	A	V	F	I	F	Y	V	P	14
50	249	V	F	I	F	Y	V	P	F	I	14
51	251	I	F	Y	V	P	F	I	G	L	14
52	257	I	G	Γ	S	М	V	Н	R	F	14
53	268	R	R	D	S	P	L	P	V	I	14
54	273	L	P	٧	Ι	L	A	N	Ι	Y	14
55	29	L	A	F	P	L	С	s	L	Y	13
56	33	L	C	S	L	Y	L	1	Α	v	13
57	55	Н	s	L	Н	E	P	М	Y	1	13
58	67	М	L	S	G	I	D	I	L	I	13
59	80	М	P	K	М	L	Α	I	F	W	13
60	95	Q	F	D	Α	C	L	L	Q	I	13
61	98	Α	C	L	L	Q	Ι	F	Α	I	13
62	104	F	A	I	Н	S	L	S	G	M	13
											75

HLA-B*5101 nonomers (SEQ ID NOS 2064-2132, respectively in order of appearance)

score										Pos	
score	9	8	7	6	5	4	3	2	1	103	
13	G	R	V	V	A	Α	V	G	I	146	63
13	A	Α	G	R	V	V	Α	A	V	148	64
13	L	P	Α	M	L	A	Α	G	R	153	65
13	\mathbf{T}	G	F	Α	K	Α	Q	A	E	233	66
13	I	F	V	Α	. C	V.	Н	s	V	243	67
13	I	Ė	K	T	K	V	G	Y	V	292	68
. 13	т	R	0	R	Т	E	K	т	К	296	69

Table XXVII, beginning at page 201, line 1, has been amended as follows:

Table XXVII:

HLA Class I decamers

HLA-A1	deca	mers (SEQ	ID	NOS
2133-21	53,	respecti	vely	<u>in</u>

	order											
	Pos	1	2	3	4	5	6	7	8	9	0	score
1	191	С	D	D	Ι	R	٧	N	V	v	Y	27
2	244	S	H	V	C	Α	V	F	Ι	F	Y	24
3	40	Α	V	L	G	N	L	$\underline{\mathbf{T}}$	I	I	Y	21
4	284	V	$\underline{\mathbf{P}}$	P	V	L	N	P	I	V	Y	21
5	116	V	Ļ	L	A	M	Α	F	D	R	Y	20
6	28	W	Ŀ	A	F	P	\mathbf{L}	\underline{c}	S	L	Y	18
7	297	T	K	E	Ι	R	Q	$\underline{\mathbf{R}}$	I	L	R	17
8	21	G	Ē	E	E	Α	Q	F	W	L	Α	16
9	22	L	\mathbf{E}	E	A	Q	F	M	L	A	F	16
10	52	R	T	E	Н	S	L	H	Ε	P	М	16
11	53	T	E	H	S	L	Н	$\underline{\mathbf{E}}$	P	M	Y	16
12	57	L	$\underline{\mathbf{H}}$	E	P	М	Y	I	F	L	С	16
13	111	G	M	E	s	T	V	$\overline{\mathbf{L}}$	L	A	M	16
14	272	P	$\underline{\mathbf{L}}$	P	V	I	L	<u>A</u>	N	I	Y	16
15	1	M	$\overline{\Lambda}$	D	P	N	G	N	E	s	s	15
16	4	P	$\overline{\mathbf{N}}$	G	N	E	S	S	A	T	Y	15
17	121	Α	$\underline{\mathbf{F}}$	D	R	Y	V	A	Ι	С	Н	15
18	171	С	R	S	N	Ι	L	\underline{s}	Н	s	Y	15
19	211	L	$\underline{\mathtt{D}}$	s	L	L	I	S	F	s	Y	15
20	8	E	\underline{s}	S	Α	T	Y	$\underline{\underline{F}}$	Ι	L	Ι	13
21	190	Α	\underline{c}	D	D	I	R	$\overline{\Lambda}$	N	v	V	13

HLA-A*0201 decamers (<u>SEQ ID</u> NOS 2154-2253, respectively

	<u>in</u>	orde	r	of	a	pр	ea	ra	nc	<u>e)</u>			
	Pc	s	1	2	3	4	5	6	7	8	9	0	score
1	2	21	L	L	Ι	L	K	T	V	L	G	L	30
2	1	.00	L	L	Q	1	F	A	I	Н	s	L	29
3	2	82	L	L	V	P	P	<u>v</u>	L	N	P	Ι	27
4	2	:05	1	I	s	Α	Ι	G	L	D	s	L	26
5	2	13	s	L	L	I	S	F	s	Y	L	L	25

HLA-A*0201 decamers(<u>SEQ ID</u> NOS 2154-2253, respectively

	in ord	er	ο£	a	pp	ea	ra	nc	e)			
	Pos	1	2	3	4	5	6	7	8	9	0	score
6	56	S	L	Н	Ε	P	M	Y	I	F	L	24
7	62	Y	I	F	L	С	М	L	S	G	I	24
8	108	S	L	S	G	М	E	S	Т	v	L	24
9	117	L	L	Α	M	Α	F	D	R	Y	V	24
10	131	P	L	R	Н	Α	T	V	L	T	L	24
11	137	v	L	Т	L	P	R	V	Т	K	I	24
12	215	L	I	S	F	S	Y	L	L	I	L	24
13	38	L	I	A	V	L	G	N	L	T	I	23
14	41	V	L	G	N	L	Т	I	Ι	Y	I	23
15	156	Α	L	М	Α	P	L	P	V	F	1	23
16	193	D	I	R	V	N	V	V	Y	G	L	23
17	214	L	L	1	S	F	S	Y	L	L	I	23
18	32	P	L	С	s	L	Y	L	Ι	A	v	22
19	119	Α	M	Α	F	D	R	Y	V	Α	I	22
20	237	K	A	F	G	Т	C	V	s	н	V	22
21	275	v	I	L	Α	N	I	Y	L	L	v	22
22	85	Α	I	F	W	F	N	s	Т	т	I	21
23	139	\mathbf{T}	L	P	R	v	Т	K	Ι	G	v	21
24	202	L	I	v	I	I	S	Α	Ι	G	L	21
25	13	Y	F	Ι	L	Ι	G	L	P	G	L	20
26	16	L	I	G	L	Р	G	L	Е	E	Α	20
27	29	L	Α	F	Р	L	C	s	L	Y	L	20
28	142	R	v	Т	K	Ι	G	v	Α	Α	v	20
29	148	V	A	Α	v	v	R	G	Α	Α	L	20
30	167	Q	L	Р	F	C	R	S	N	I	L	20
31	180	Y	С	L	Н	Q	D	v	М	ĸ	L	20
32	222	L	I	L	K	T	v	L	G	Ļ	T	20
33	240	G	т	С	v	s	H	V	C	A	v	20
34	248	A	v	F	I	F	Y	v	P	F	I	20
35	250	F	I	F	Y	v	P	F	I	G	L	20
36	271	s	P	L	P	v	Ī	L	Ā	N	I	20
37	279	N	I	Y	L	L	v	P	P	v	L	20
38	304	I	L	R	L	F	H	v	A	T	Н	20
39	10	S	A	Т	Y	F	ï	L	I	G	L	19
40	15	I	L	ī	G	L	P P	G	L	E	E	19
41	27	F	W	L	A	F	P	L	C	s	L	19
42	35	s	L	Y	L	I	Ā	v	L	G	N	19
43	37	Y	L	I	A	v	L	G	N	L	Т	19
44	44	N	L	T	I	I	Y	I	v	R	T	19
45	64	F		C	M	L	S	G	I	D	ī	19
46	83	М	L	Ā	I	F	≃ W	F	N	s	Т	19
47	159	A	P	L	P	v	F	I	K	Q	L	19
48	189	L	A	C	D	D	Ĩ	R	v	N	v	19
49	207	s	A	I	G	L	Ē D	s	L	L	I	19
50	253	Y	v	P	F	I	G	L	s	м	v	19
51	276	I	L	A	N	I	Y	L	L	v	P	19
52	281	Y	L	L	V	Р	P	A P	L	N	Þ	19
53	283	L	v	Р	P	V	L	N	Р	I	V	19
54	286	P	v	L	N	P	ī	V	Y	G	v	19
55	33	L	c	s	L	Y	L	I	A	v	L	18
	55	_	_	J	_	_	=	_	. 1	٠	_	77
												//

HLA-A*0201	decamers	(SEQ ID
NOS 2154-22	253, resp	ectively

	in or		of	<u>ээ</u>		ea		nc	-	<u> </u>	<u>+ y</u>	
	Pos	1	2	3	4	5	6	7	8	9	0	score
56	36	\mathbf{L}	Y	L	I	Α	v	L	G	N	L	18
57	39	I	A	V	L	G	N	L	T	I	Ι	18
58	42	L	G	N	L	Т	I	I	Y	I	V	18
59	66	С	M	L	S	G	I	D	1	L	I	18
60	111	G	M	Ε	S	\mathbf{T}	\underline{v}	L	L	A	М	18
61	128	I	C	Н	P	L	$\underline{\underline{R}}$	Н	Α	T	V	18
62	134	Н	A	Т	V	L	$\underline{\underline{T}}$	L	P	R	V	18
63	154	G	A	A	L	M	$\underline{\underline{A}}$	P	L	P	V	18
64		L	M	A	P	.L	<u>P</u>	V	F	I	K	18
65		Α	С	D	D	Ι	R	V	N	V	V	18
66		G	L	Т	R	E	<u>A</u>	Q	A	K	A	18
67		Н	V	С	A	V	$\frac{\mathbf{F}}{\mathbf{F}}$	I	F	Y	V	18
68		P	V	Ι	L	A	$\overline{\mathbf{N}}$	Ι	Y	L	L	18
69		A	N	Ι	Y	L	F	V	Р	P	V	18
70		Ι	٧	Y	G	V	K	T	K	E	I	18
71		K	E	I	R	Q	R	I	L	R	L	18
72		I	Y	Ι	V	R	$\frac{\mathbf{T}}{2}$	E	H	S	L	17
73		L	C	M	L	S	G	I	D	I	L	17
74		М	L	S	G	I	D	Ι	L	I	S	17
75		L	I	S	T	S	<u>s</u>	M	P	K	M	17
76		s	T	Т	I	Q	F	D	A	C	L	17
77		I	Q	F	D	A	<u>C</u>	L	L	Q	I	17
78		K	L	A	C	D	D	I	R	v	N	17
79		N	V	V	Y	G	$\frac{r}{\Gamma}$	I	V	I	I	17
80		Y	G	L	I	V	Ī	I	S	A	I	17
81 82		F V	S L	Y G	L	L T	Ī	L E	K A	T Q	V	17
83		R	I	L	R	L	R F	Н	V	A	A T	17 17
84		G	L	Е	E	A	Q	F	W	L	A	16
85		Т	Т	I	Q	F	D	A	C	L	L	16
86		D	A	C	L	L	Q	I	F	A	I	16
87		A	I	C	Н	P	≚ L	R	Н	A	Т	16
88		v	т	к	I	G	v	A	A	v	v	16
. 89		R	v	N	v	v	Ÿ	G	L	I	v	16
90		Y	L	L	I	L	K	Т	v	L	G	16
91		ĸ	T	ĸ	E	I	R	Q	R	I	L	16
92		G	L	P	G	L	E	Ē	A	Q	F	15
93		A	F	P	L	C	S	L	Y	L	I	15
94		v	A	Ι	С	Н	P	L	R	н	A	15
95		К	I	G	v	Α	Ā	v	v	R	G	15
96		s	N	I	L	s	H	s	Y	C	L	15
97		G	L	I	V	I	1	s	A	I	G	15
98		A	I	G	L	D	s	L	L	I	s	15
99		G	L	D	s	L	$_{ m L}$	I	s	F	S	15
100		K	R	R	D	S	P	ь	P	v	Ι	15
		_					_					

HLA-A*0203 decamers (SEQ ID NOS 2254-2301, respectively

HLA-A*0203 decamers (SEQ ID NOS 2254-2301, respectively in order of appearance)

	in or	ler	of	a	pp	ea	ra	nc	e)			
	Pos	1	2	3	4	5	6	7	8	9	0	score
1	141	P	R	v	\mathbf{T}	K	Ι	G	V	A	Α	19
2	147	G	V	A	Α	V	V	R	G	A	Α	19
3	112	М	E	s	Т	٧	L	L	Α	M	Α	18
4	227	V	L	G	L	Т	R	E	Α	Q	Α	18
5	229	G	L	т	R	E	Α	Q	Α	ĸ	Α	18
6	142	R'	v	T	K	Ι	G	v	Α	A	٧	17
7	148	V	A	Α	v	v	R	G	A	A	L	17
8	2	V	D	P	N	G	N	E	S	s	Α	10
9	16	L	I	G	L	P	G	L	E	E	Α	10
10	21	G	L	E	E	Α	Q	F	W	L	Α	1.0
11	31	F	P	L	С	S	L	Y	L	I	Α	10
12	76	s	T	S	s	М	Р	K	М	L	Α	10
13	89	F	N	s	Т	Т	Ι	Q	F	D	Α	10
14	96	F	D	A	С	L	L	Q	Ι	F	Α	10
15	110	s	G	M	Е	s	Т	V	L	L	Α	10
16	118	L	A	M	Α	F	D	R	Y	v	Α	10
17	126	V	Ā	I	С	Н	P	L	R	н	Α	10
18	140	L	P	R	v	Т	K	I	G	v	Α	10
19	146	Ι	G	v	Α	Α	v	v	R	G	Α	10
20	150	Α	v	v	R	G	Α	– A	L	м	Α	10
21	181	С	L	н	Q	D	v	_ M	K	L	А	10
22	199	V	Y	G	L	Ι	v	ī	I	s	Α	10
23	225	к	T	v	L	G	L	T	R	E	Α	10
24	239	F	G	т	С	v	S	H	V	C	Α	10
25	269	R	D	s	P	L	Р	v	Ι	L	Α	10
26	302	Q	R	I	L	R	L	F	Н	v	A	10
27	305	L	R	L	F	Н	v	Ā	Т	н	Α	10
28	3	D	P	N	G	N	E	s	s	A	т	9
29	17	I	G	L	P	G	L	E	E	A	Q	9
30	22	L	E	E	Α	Q	F	W	L	A	F	9
31	32	P	L	C	S	L	Y	L	I	A	v	9
32	77	Т	<u>=</u>	s	М	P	ĸ	M	Ь	A	I	9
33	90	N	S	T	Т	I	Q	F	D	A	C	9
34	97	D	Ā	C	L	L	Q	I	F	Α	I	9
35	111	G	M	E	s	T	v	L	L	A	M	9
36	113	E	S	T	v	L	L	= A	M	A	F	9
37	119	A	M	A	F	D	R	Y	v	A	I	9
38	127	A	I	С	Н	P	L	R	Н	A	Т	9
39	151	v	v	R	G	A	A	L	М	A	P	9
40	182	L	H	Q	D	v	М	ĸ	L	A	C	9
41	200	Y	G G	L	I	v	I	Ī	s	A	I	9
42	226	т	v	L	G	L	T	± R	E	A	Q	9
43	228	L	Ğ	L	Т	R	E	A	Q	A	K	9
44	230	L	T	R	E	A	Q	A	K	A	F	9
45	240	G	T	C	V	S	Н	v	C	A	V	9
46	270	D	s	P	L	P	V	ĭ	L	A	N	9
47	303	R	<u> </u>	L	R	L	F	H	V	A	Т	9
48		R	Ļ L			V						9
40	306	ĸ	브	F	Н	٧	A	$\underline{\mathbf{T}}$	H	A	S	9

HLA-A26 decamers (SEQ ID NOS 2302-2366, respectively in order of appearance)

	order	of	ap	рe	ar	an	ce)				
	Pos	1	2	3	4	5	6	7	8	9	0	score
1	299	E	Ι	R	Q	R	I	L	R	L	F	31
2	193	D	Ι	R	V	N	V	v	Y	G	L	29
3	250	F	I	F	Y	v	Р	F	Ι	G	L	25
4	256	F	I	G	L	s	М	V	Н	R	F	25
5	74	L	I	S	Т	s	s	М	Р	K	М	24
6	274	P	v	I	L	A	N	I	Y	L	L	24
7	18	G	L	P	G	L	E	E	A	Q	F	23
. 8	116	v	L	L	A	М	A	F	D	R	Y	23
9	205	I	I	s	A	ľ	G	L	D	s	L	23
10	221	L	L	I	Г	K	Т	V	L	G	L	23
11	230	L	Т	R	E	A	Q	A	К	A	F	23
12	13	Y	F	I	L	I	G	L	P	G	L	23
13	40	A	V	L	G	N	L	Т	I	I	Y	
14	56	S	L	Н	E	Р	М	Y	I	F	L	22
15	95		F									22
		Q		D	A	C	L	L	Q	I	F	22
16	215	L	Ι	S	F	S	Y	L	L	I	L	22
17	92	Т	T	Ι	Q	F	D	A	С	L	L	21
18	100	L	L	Q	1	F	A	I	Н	S	L	21
19	103	I	F	A	I	H	S	L	S -	G	M	21
20	296	K	Т	K	Ε	Ι	R	Q	R	Ι	L	21
21	28	W	L	A	F	Ρ	L	С	S	L	Y	20
22	131	Þ	L	R	Η	A	Т	V	L	Т	Ļ	20
23	59	Ε	P	M	Y	Ι	F	L	C	M	L	19
24	91	S	Т	Т	I	Q	F	D	A	C	\mathbf{L}	19
25	202	L	Ι	V	Ι	1	S	A	I	G	L	19
26	212	D	S	L	L	Ι	S	F	S	Y	L	19
27	272	P	L	Р	V	Ι	L	A	N	Ι	Y	19
28	279	N	I	Y	L	L	V	Р	P	V	L	19
29	52	R	Т	Е	Η	S	L	Н	E	P	М	18
30	62	Y	Ι	F	L	C	M	L	S	G	Ι	18
31	72	D	I	L	Ι	S	Т	S	S	M	P	18
32	108	S	L	S	G	М	E	S	T	V	L	18
33	113	E	S	Т	V	L	L	Α	M	A	F	18
34	151	V	v	R	G	A	A	L	M	Α	P	18
35	78	S	S	M	P	K	M	L	A	I	F	17
36	142	R	V	Т	K	Ι	G	V	Α	A	V	17
37	162	P	V	F	Ι	K	Q	L	P	F	C	17
38	164	F	I	K	Q	L	P	F	С	R	S	17
39	167	Q	L	P	F	C	R	s	И	Ι	\mathbf{L}	17
40	185	D	V	M	K	L	Α	С	D	D	1	17
41	248	Α	V	F	I	F	Y	V	Ρ	F	I	17
42	253	Y	V	P	F	1	G	L	s	М	V	17
43	45	L	Т	I	Ι	Y	Ι	V	R	T	E	16
44	145	K	Ι	G	V	Α	Α	V	V	R	G	16
45	198	V	V	Y	G	L	Ι	v	Ι	1	S	16
46	203	I	V	Ι	1	s	Α	Ι	G	L	D	16
47	209	Ι	G	L	D	s	L	L	I	s	F	16
48	213	s	L	L	I	s	F	s	Y	L	L	16
49	255	P	F	I	G	L	s	M	V	Н	R	16
50	264	R	F	s	ĸ	R	R	D	s	P	L	16
		-										80
												00

HLA-A2	26 0	le	car	er	s (:	SEQ	ID	NOS
2302-2	2366	5,	re	sp	ect	tive	ely	in
order	of	aj	ppe	ar	and	ce)		

				_				<u> </u>				
	Pos	1	2	3	4	5	6	7	8	9	0	score
51	294	G	V	K	\mathbf{T}	K	Ε	I	R	Q	R	16
52	16	L	Ι	G	L	P	G	L	E	Е	Α	15
53	80	M	P	K	М	L	Α	I	F	W	F	15
54	114	S	Τ,	V	L	L	Α	М	A	F	D	15
55	155	Α	Α	L	М	A	P	L	P	V	F	15
56	159	A	P	L	P	V	F	Ι	K	Q	L	15
57	174	N	Ι	L	S	Н	S	Y	С	L	Н	15
58	197	N	V	V	Y	G	L	I	V	Ι	I	15
59	210	G	L	D	S	L	L	I	S	F	S	15
60	214	L	L	Ι	S	F	S	Y	L	L	I	15
61	222	L	Ι	L	K	T	V	L	G	L	T	15
62	240	G	T	C	V	S	Н	V	C	Α	V	15
63	247	C	A	V	F	I	F	Y	V	P	F	15
64	286	P	V	L	N	P	Ι	V	Y	G	V	15
65	298	K	Е	I	R	Q	R	Ι	L	R	L	15

HLA-A3 decamers (SEQ ID NOS 2367-2432, respectively in

	order	of	ap	рe	ar		ce		<u>- y</u>				
	Pos	1	2	3	4	5	6	<u>-</u> 7	8	9	0	score	
1		т	v	L	т	L	P	R	V	T	К	31	
2	287	v	L	N	Р	Ι	v	Y	G	v	K	28	
3	223	I	L	K	Т	v	$_{\rm L}$	G	L	т	R	27	
4	304	I	L	R	L	F	H	v	Α	т	Н	27	
5 73 I L <u>I</u> S T <u>S</u> <u>S</u> M P K 26													
6	15	I	L	I	G	L	P	G	L	Е	E	23	
7	40	Α	v	L	G	N	L	T	Ι	I	Y	23	
8 150 A V V R G A A L M A 23													
9 258 G L S M V H R F S K 23													
10	18	G	L	P	G	L	$\underline{\mathbf{E}}$	E	A	Q	F	22	
11	303	R	I	$\underline{\mathtt{L}}$	R	L	$\underline{\mathbf{F}}$	$\underline{\mathbf{H}}$	V	A	\mathbf{T}	22	
12	276	I	L	A	N	Ι	$\underline{\underline{Y}}$	$\underline{\mathbf{L}}$	L	V	Р	21	
13	28	M	L	A	F	P	$\overline{\Gamma}$	$\underline{\mathtt{C}}$	S	L	Y	20	
14	115	Т	v	$\underline{\mathbf{L}}$	L	A	M	A	F	D	R	20	
15	116	V	L	Ŀ	Α	М	A	F	D	R	Y	20	
16	125	Y	v	A	I	С	$\underline{\underline{H}}$	P	L	R	Н	20	
17	131	P	L	R	Н	Α	$\underline{\mathtt{T}}$	Ā	L	T	L	20	
18	144	Т	K	I	G	V	A	A	V	v	R	20	
19	156	Α	L	M	Α	P	L	$\underline{\mathbf{P}}$	V	F	Ι	20	
20	195	R	v	N	٧	V	$\underline{\underline{Y}}$	G	L	I	V	20	
21	35	S	L	$\underline{\underline{Y}}$	L	I	A	<u>v</u>	L	G	N	19	
22	272	P	L	P	V	Ι	$\overline{\Gamma}$	A	N	I	Y	19	
23	37	Y	L	I	A	V	$\overline{\Gamma}$	$\underline{\mathbf{G}}$	N	L	Т	18	
24	49	Y	I	\underline{V}	R	Т	E	H	S	L	Н	18	
25	50	I	v	R	T	E	$\overline{\mathbf{H}}$	s	L	H	E	18	
26	108	S	L	\underline{s}	G	M	E	s	T	v	L	18	
27	142	R	v	T	K	Ι	G	V	Α	A	V	18	
28 188 K L A C D D I R V N 18													
29 279 N I Y L L V P P V L 18													
30	291	I	v	Y	G	V	K	T	K	E	I	18	
												81	

HLA-A3 decamers(SEQ ID NO	S
2367-2432, respectively	'n
order of appearance)	_

	Pos	1	2	3	4	5	6	7	8	9	0	score
31	294	G	V	K	Т	K	E	I	R	Q	R	18
32	46	Т	I	I	Y	1	V	R	T	E	Н	17
33	102	Q	I	F	Α	I	H	S	L	S	G	17
34	151	V	v	R	G	A	A	$\overline{\mathbf{r}}$	М	A	P	17
35	179	S	Y	$\overline{\mathbf{c}}$	L	Н	\underline{Q}	$\underline{\mathbf{D}}$	V	M	K	17
36	203	I	v	Ī	I	S	A	I	G	L	D	17
37	204	V	I	I	S	A	I	$\underline{\mathbf{G}}$	L	D	s	17
38	220	Y	L	$\underline{\mathbf{L}}$	I	\mathbf{L}	K	$\underline{\mathbf{T}}$	V	L	G	17
39	221	L	L	<u>I</u>	L	K	$\underline{\mathbf{T}}$	V	L	G	L	17
40	227	V	L	$\underline{\mathbf{G}}$	\mathbf{L}	T	\underline{R}	$\underline{\mathbf{E}}$	A	Q	Α	17
41	242	C	V	\underline{s}	Н	V	\underline{C}	<u>A</u>	V	F	I	17
42	289	N	P	<u>I</u>	V	Y	$\underline{\mathbf{G}}$	V	K	T	K	17
43	38	L	I	$\underline{\mathbf{A}}$	V	L	G	N	L	T	Ι	16
44	85	A	I	$\underline{\mathbf{F}}$	W	F	Ŋ	\underline{s}	T	T	Ι	16
45	147	G	v	A	Α	V	V	R	G	A	Α	16
46	198	V	V	Y	G	L	I	$\underline{\mathbf{v}}$	Ι	I	s	16
47	201	G	L	I	V	I	Ī	\underline{s}	Α	I	G	16
48	214	L	L	I	S	F	$\underline{\mathbf{s}}$	$\underline{\underline{Y}}$	L	L	Ι	16
49	226	T	V	ī	G	L	$\underline{\mathbf{T}}$	R	E	A	Q	16
50	228	L	G	Ŀ	T	R	$\underline{\mathbf{E}}$	$\underline{\mathbf{A}}$	Q	A	K	16
51	229	G	L	T	R	E	$\underline{\mathbf{A}}$	\underline{Q}	A	K	А	16
52	1	M	v	$\overline{\mathbf{D}}$	P	N	$\underline{\underline{G}}$	N	E	S	S	15
53	44	N	L	$\underline{\mathbf{T}}$	Ι	Ι	$\underline{\underline{Y}}$	Ī	V	R	\mathbf{T}	15
54	47	I	I	Y	Ι	V	R	$\underline{\mathbf{T}}$	E	H	s	15
55	67	М	L	\underline{s}	G	Ι	$\underline{\underline{D}}$	I	L	I	S	15
56	72	D	Ι	ഥ	I	S	$\underline{\mathbf{T}}$	$\underline{\mathbf{s}}$	S	M	Р	15
57	99	С	L	$\underline{\mathtt{L}}$	Q	Ι	F	A	I	H	S	15
58	105	Α	I	H	S	L	$\underline{\mathbf{S}}$	$\underline{\mathbf{G}}$	M	E	S	15
59	145	K	I	$\underline{\mathbf{G}}$	٧	A	$\underline{\underline{A}}$	$\overline{\Lambda}$	V	R	G	15
60	175	I	L	\underline{s}	H	S	Y	\underline{C}	Γ	H	Q	15
61	191	C	D	$\underline{\mathbf{D}}$	Ι	R	$\underline{\mathtt{v}}$	N	V	v	Y	15
62	208	Α	I	$\underline{\mathbf{G}}$	L	D	$\underline{\underline{s}}$	$\underline{\mathbf{r}}$	L	I	S	15
63	275	V	I	$\overline{\Gamma}$	A	N	Ī	$\underline{\underline{Y}}$	L	L	V	15
64	281	Y	L	$\underline{\underline{\mathbf{r}}}$	V	P	$\underline{\underline{P}}$	$\underline{\underline{v}}$	L	N	P	15
65	299	E	I	$\underline{\underline{R}}$	Q	R	$\underline{\mathtt{I}}$	Ī	R	L	F	15
66	306	R	L	$\underline{\underline{F}}$	Н	V	$\underline{\underline{A}}$	$\underline{{\mathtt T}}$	Н	A	S	15

HLA-B*0702 decamers (SEQ ID NOS 2433-2492, respectively

	in ord											
	Pos	1.	2	3	4	5	6	7	8	9	0	score
1.	159	Α	P	L	P	V	F	I	K	Q	L	23
2	59	E	P	M	Y	I	F	L	C	M	L	22
3	273	L	P	V	Ι	L	Α	N	Ι	Y	L	20
4	3	D	P	N	G	N	E	S	S	A	\mathbf{T}	19
5	130	Н	₽	L	R	Н	Α	Т	V	L	\mathbf{T}	19
6	140	L	P	R	V	T	K	Ι	G	v	Α	19
7	161	L	P	V	F	Ι	K	Q	L	P	F	19
8	31	F	P	L	C	S	L	Y	L	I	Α	18
9	271	S	P	L	Ρ	V	Ι	L	Α	N	I	18
			82									

HLA-B*0702 decamers (SEQ ID NOS 2433-2492, respectively

	in ord	er	of	a	pp	ea	ra	nc	e)			
	Pos	1	2	3	4	5	6	7	8	9	0	score
10	80	М	Р	K	М	L	Α	I	F	W	F	16
11	108	S	L	S	G	М	Е	s	Т	v	L	16
12	131	P	L	R	Н	Α	Т	v	L	т	L	15
13	264	R	F	S	K	R	R	D	s	P	L	15
14	33	L	C	s	L	Y	L	I	A	v	L	14
15	109	L	s	G	М	E	s	Т	V	L	L	14
16	152	v	R	G	A	A	L	М	A	P	L	14
17	205	I	I	s	A	1	G	L	D	s	L	14
18	215	L	I	s	F	s	Y	L	L	I	L	14
19	268	R	R	D	s	P	L	P	v	I	L	14
20	29	L	A	F	P	L	С	s	L	Y	L	13
21	148	V	A	A	V	V	R	G	А	A	L	13
22	156	A	L	М	A	P	L	P	v	F	I	
23	193	D	I	R	V			V				13
						N	V		Y	G	L	13
24	221	L	L	I	L	K	T	V	L	G	L	13
25	298	K	E	Ι	R	Q	R	I	L	R -	L	13
26	7	N	E	S	S	A	T	Y	F	I	L	12
27	19	L	P	G	L	Е	E	A	Q	F	W	12
28	24	E	Α	Q	F	W	L	A	F	P	L	12
29	119	A	M	A	F	D	R	Y	V	A	Ι	12
30	129	C	Н	P	L	R	Н	A	T	v	L	12
31	206	I	S	A	Ι	G	Ь	D	S	L	L	12
32	219	S	Y	L	L	Ι	\mathbf{L}	K	T	V	L	12
33	279	N	Ι	Y	L	L	V	P	P	v	L	12
34	285	P	P	V	L	N	Р	Ι	V	Y	G	12
35	8	E	S	S	Α	T	Y	F	I	L	I	11
36	13	Y	F	1	L	I	G	L	P	G	L	11
37	27	F	W	L	Α	F	P	L	C	S	L	11
38	48	I	Y	Ι	V	R	T	E	Н	s	L	11
39	56	S	L	Н	Е	P	М	Y	Ι	F	L	11
40	65	L	C	М	L	s	G	Ι	D	r	L	11
41	75	I	s	T	S	S	M	Ρ	K	M	L	11
42	77	т	s	S	М	P	K	М	L	A	1	11
43	91	S	T	Т	Ι	Q	F	D	Α	C	L	11
44	123	D	R	Y	v	A	Ι	С	Н	P	L	11
45	142	R	v	Т	K	I	G	ν	Α	A	V	11
46	180	Y	C	L	Н	Q	D	v	М	ĸ	L	11
47	190	Α	C	D	D	Ι	R	ν	N	v	v	11
48	212	D	s	L	L	I	s	F	S	Y	\mathbf{L}	11
49	234	Α	Q	Α	K	Α	F	G	Т	С	v	11
50	242	C	v	S	Н	v	С	Α	V	F	I	11
51	248	Α	v	F	I	F	Y	v	P	F	Ι	11
52	250	F	I	F	Y	v	Р	F	I	G	L	11
53	254	v	P	F	I	G	L	s	М	v	H	11
54	266	S	ĸ	R	R	D	s	P	L	P	v	11
55	267	K	R	R	Đ	s	P	L	P	v	I	11
56	269	R	D	s	P	L	P	v	ī	L	A	11
57	278	Α	N	I	Y	L	L	v	P	P	v	11
58	284	V	P	P	v	L	N	P	I	v	Y	11
59	289	N	P	I	v	Y	G	v	K	т	K	11
-						-	-		-	-		83
												0.5

HLA-B*0702 decamers (SEQ ID

NOS 2433-2492, respectively

in order of appearance)

Pos 1 2 3 4 5 6 7 8 9 0 score

60 296 KTKEIRQRIL 11

Table XXVIII, beginning at page 205, line 1, has been amended as follows:

Table XXVIII:

HLA Class II Epitopes (sample 15-mer length)

$\frac{(\text{SEQ ID NOS 2493-2595, respectively in order of appearance})}{\text{HLA-DRB1*0101 } 15\text{-mers}}$

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	200	Y	G	L	I	V	I	I	s	A	1	G	L	D	s	L	36
2	68	L	S	G	I	D	I	L	Ι	s	\mathbf{T}	s	s	М	P	K	34
3	62	Y	Ι	F	L	С	M	L	S	G	I	D	Ι	L	I	S	33
4	103	I	F	Α	I	Н	S	L	s	G	М	E	S	Т	V	L	32
5	45	L	T	I	I	Y	I	V	R	T	E	Н	s	L	Н	E	31
6	193	D	I	R	v	N	v	V	Y	G	L	Ι	V	1	Ι	S	31
7	277	L	Α	N	I	Y	L	\mathbf{L}	V	P	P	V	L	N	P	1	31
8	97	D	Α	C	L	L	Q	Ι	F	A	I	Н	S	L	s	G	30
9	106	I	Н	S	L	S	G	М	\mathbf{E}	s	Т	V	L	L	Α	M	30
10	240	G	Т	С	v	S	Н	V	С	A	V	F	I	F	Y	V	30
11	10	S	Α	\mathbf{T}	Y	F	I	L	Ι	G	L	Р	G	L	\mathbf{E}	E	29
12	289	N	Р	Ι	v	Y	G	V	K	T	K	Е	Ι	R	Q	R	29
13	11	A	Т	Y	F	I	L	I	G	L	P	G	L	E	E	Α	28
14	250	F	Ι	F	Y	V	P	F	1	G	\mathbf{L}	S	M	V	Н	R	27
15	140	L	P	R	V	Т	K	I	G	v	Α	Α	V	V	R	G	26
16	183	H	Q	D	V	М	K	L	A	С	D	D	1	R	V	N	26
17	217	S	F	S	Y	L	L	Ι	L	K	\mathbf{T}	V	L	G	\mathbf{L}	Т	26
18	16	L	I	G	L	P	G	L	E	Е	A	Q	F	W	\mathbf{L}	Α	25
19	24	E	Α	Q	F	M	L	A	F	P	L	C	S	L	Y	L	25
20	36	L	Y	L	I	Α	v	L	G	N	L	T	Ι	1	Y	Ι	25
21	70	G	Ι	D	I	L	I	S	T	S	S	M	Р	K	М	L	25
22	111	G	M	E	S	Т	v	L	\mathbf{L}	Α	M	A	F	D	R	Y	25
23	148	v	A	A	V	V	R	G	Α	Α	L	M	A	Ъ	L	P	25
24	162	P	V	F	Ι	K	Q	L	Р	F	С	R	S	N	Ι	L	25
25	197	N	V	V	Y	G	L	Ι	V	I	Ι	S	Α	I	G	L	25
26	211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	25
27	218	F	S	Y	L	L	I	L	K	T	V	L	G	L	Т	R	25
28	13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	24
29	30	A	F	P	L	C	S	L	Y	L	I	A	V	L	G	N	24
30	39	I	A	V	L	G	N	L	Т	I	I	Y	Ι	V	R	T	24
31	77	T	S	S	M	P	K	M	L	A 	I	F	W	F	N	S	24
32	85	A	I	F	W	F	N	S	Т	T	I	Q	F	D	A	С	24
33	137	v	L	T	L	P	R	V	T	K	I	G	V	Α	A	V	24
34	151	V -	V	R	G	A	A	L	M	A	Þ	L	P	V	F	I	24
35	161	L	P	V	F	Ι	K	Q	L	P 	F	C	R	S	N	I	24
36	196	v	N	V	V	Y	G	L	I	v	Ι	Ι	S	A	I	G	24

HLA-DRB1*0101 15-mers

	Pos																score
		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	
37	202	L	Ι	V	I	1	S	Α	1	G	L	D	S	L	L	Ι	24
38	208	A	Ι	G	L	D	S	L	L	Ι	S	F	S	Y	L	L	24
39	248	Α	V	F	I	F	Y	V	Ρ	F	Ι	G	L	S	M	V	24
40	251	I	F	Y	V	Ρ	F	Ι	G	L	S	M	V	Н	R	F	24
41	83	M	L	A	I	F	W	F	N	S	\mathbf{T}	Т	I	Q	F	D	23
42	101	L	Q	Ι	F	Α	I	Н	S	L	S	G	M	Ε	S	Т	23
43	165	I	K	Q	L	Р	F	С	R	S	И	I	L	S	Н	S	23
44	203	I	V	I	I	S	A	I	G	L	D	S	\mathbf{L}	L	Ι	S	23
45	221	L	\mathbf{L}	1	L	K	T	V	L	G	L	Т	R	E	Α	Q	23
46	278	A	N	Ι	Y	L	L	V	Р	P	V	L	И	P	I	V	23
47	27	F	W	\mathbf{L}	A	F	P	L	C	S	\mathbf{L}	Y	L	I	А	V	22
48	35	S	L	Y	L	Ι	A	V	\mathbf{L}	G	N	\mathbf{L}	\mathbf{T}	Ι	Ι	Y	22
49	61	M	Y	Ι	F	L	C	М	L	S	G	I	D	I	L	Ι	22
50	65	L	C	М	L	S	G	Ι	D	I	L	I	S	\mathbf{T}	S	s	22
51	80	M	P	K	M	L	A	Ι	F	W	F	N	S	\mathbf{T}	\mathbf{T}	I	22
52	145	K	I	G	v	Α	A	V	V	R	G	Α	Α	L	М	A	22
53	146	Ī	G	V	Α	Α	v	V	R	G	Α	Α	L	М	Α	Р	22
54	154	G	Α	Α	L	М	A	P	L	P	V	F	Ι	K	Q	L	22
55	205	I	I	s	A	I	G	L	D	s	L	L	I	S	F	s	22
56	243	v	S	Н	v	С	Α	V	F	I	F	Y	V	Р	F	Ι	22
57	270	D	S	P	L	Р	v	I	L	A	N	Ι	Y	L	L	V	22
58	274	P	V	1	L	Α	N	I	Y	L	L	V	P	P	V	L	22
59	281	Y	L	L	v	Р	P	V	L	N	P	I	V	Y	G	V	22
60	34	C	S	L	Y	L	I	Α	V	L	G	N	L	\mathbf{T}	Ι	Ι	21
61	69	s	G	1	D	Ι	L	I	s	T	s	s	М	Р	K	М	21
62	152	v	R	G	Α	Α	L	М	Α	P	L	Р	v	F	I	K	21
63	299	E	Ι	R	Q	R	I	L	R	L	F	Н	V	Α	\mathbf{T}	Н	21
64	100	L	L	Q	I	F	A	1	Н	s	L	s	G	M	Ε	s	20
65	135	Α	Т	V	L	т	L	P	R	v	Т	K	I	G	V	Α	20
66	141	P	R	V	т	K	I	G	V	A	Α	V	V	R	G	Α	20
67	191	C	D	D	I	R	v	N	V	v	Y	G	L	Ι	v	1	20
68	199	v	Y	G	L	I	v	I	Ι	s	Α	1	G	L	D	s	20
69	262	v	Н	R	F	s	ĸ	R	R	D	S	Р	L	Р	V	1	20
70	271	s	Р	L	P	V	I	L	Α	N	I	Y	L	L	v	P	20
71	28	W	L	Α	F	Р	L	С	s	L	Y	L	I	Α	V	L	19
72	58	н	E	P	M	Y	I	F	L	C	М	L	s	G	I	D	19
73	59	E	P	M	Y	Ι	F	L	С	M	L	s	G	I	D	I	19
74	60	P	М	Y	I	F	L	C	М	L	s	G	I	D	I	L	19
75	98	A	С	L	L	Q	I	F	Α	I	Н	S	L	S	G	М	19
76	215	L	I	S	F	S	Y	L	L	I	L	K	\mathbf{T}	V	L	G	19
77	219	s	Y	· L	L	I	L	K	Т	v	L	G	L	Т	R	E	19
78	228	L	G	L	T	R	E	Α	Q	Α	K	Α	F	G	Т	C	19
79	232	R	Е	Α	Q	Α	ĸ	A	F	G	Т	C	V	S	Н	V	19
80	246	v	С	A	v	F	I	F	Y	v	P	F	Ι	G	L	s	19
81	297	T	K	E	I	R	Q	R	Ι	L	R	L	F	Н	V	Α	19
82	3	D	P	N	G	N	E	s	s	A	Т	Y	F	I	L	I	18
83	14	F	I	L	I	G	L	Р	G	L	E	E	Α	Q	F	W	18
84	25	A	Q	F'	W	L	A	F	P	L	С	S	L	Y	L	Ι	18
85	42	L	G	N	L	Т	I	Ι	Y	I	V	R	Т	E	Н	s	18
86	46	т	I	I	Y	I	v	R	Т	E	Н	s	L	Н	Е	P	18
87	78	s	S	М	P		М		Α	I	F	W	F	N	s	T	18
														8	35		

HLA-DRB1*0101 15-mers

	Pos																
	FUS	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
88	84	L	Α	Ι	F	W	F	N	S	\mathbf{T}	Т	1	Q	F	D	Α	18
89	89	F	N	S	T	Т	I	Q	F	D	Α	С	L	\mathbf{L}	Q	Ι	18
90	93	T	Ι	Q	F	D	A	С	L	L	Q	I	F	Α	I	Н	18
91	115	T	V	L	L	Α	M	Α	F	D	R	Y	V	Α	I	С	18
92	119	A	М	Α	F	D	R	Y	V	A	Ι	C	Н	Р	L	R	18
93	127	A	Ι	С	H	P	L	R	Н	A	\mathbf{T}	V	L	\mathbf{T}	L	P	18
94	129	C	Н	Р	L	R	н	Α	Т	v	L	\mathbf{T}	L	Р	R	V	18
95	147	G	V	Α	A	V	v	R	G	A	Α	L	М	Α	Р	L	18
96	149	A	Α	V	v	R	G	Α	Α	L	M	А	P	L	Р	V	18
97	216	I	S	F	s	Y	L	L	Ι	L	K	\mathbf{T}	V	L	G	L	18
98	227	v	L	G	L	Т	R	E	Α	Q	Α	K	A	F	G	Т	18
99	249	v	F	I	F	Y	v	P	F	I	G	\mathbf{L}	S	M	V	Н	18
100	253	Y	V	P	F	I	G	L	S	M	V	Н	R	F	S	K	18
101	284	v	P	Ρ	v	L	N	P	I	v	Y	G	V	K	Т	K	18
102	286	P	V	L	N	Р	I	V	Y	G	V	K	Т	K	E	I	18
103	303	R	Ι	L	R	L	F	Н	V	Α	\mathbf{T}	Н	Α	S	Е	P	18

HLA-DRB1*0301 (DR17) 15-mers (SEQ ID NOS 2596-2671, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	. 3	4	5	score
1	16	L	Ι	G	L	P	G	L	E	E	A	Q	F	W	L	Α	26
2	206	I	s	Α	I	G	L	D	S	L	L	I	s	F	s	Y	23
3	91	S	$^{\circ}\mathbf{T}$	\mathbf{T}	I	Q	F	D	Α	C	\mathbf{L}	L	Q	I	F	Α	22
4	117	L	L	A	M	Α	F	D	R	Y	V	Α	I	С	Н	P	22
5	38	L	Ι	Α	v	L	G	N	L	T	I	I	Y	I	V	R	21
6	179	S	Y	C	L	Н	Q	D	V	M	K	L	Α	С	D	D	21
7	211	L	D	S	L	L	I	S	F	s	Y	L	L	Ι	L	K	21
8	219	S	Y	L	L	I	L	K	Т	v	L	G	L	Т	R	E	21
9	272	P	L	P	v	1	L	Α	N	I	Y	L	L	V	P	P	21
10	26	Q	F	W	L	А	F	Р	\mathbf{L}	С	s	L	Y	L	I	Α	20
11	114	S	Т	V	L	L	A	М	Α	F	D	R	Y	V	Α	I	20
12	129	C	Н	P	L	R	H	Α	Т	V	L	Т	L	P	R	V	20
13	134	H	A	\mathbf{T}	v	L	T	L	P	R	V	\mathbf{T}	K	Ι	G	V	20
14	186	v	М	K	L	А	C	D	D	I	R	V	N	V	V	Y	20
15	200	Y	G	L	I	V	I	I	S	Α	Ι	G	\mathbf{L}	D	S	\mathbf{L}	20
16	270	D	S	P	L	Р	v	Ι	L	A	N	Ι	Y	\mathbf{L}	L	V	20
17	297	T	K	E	I	R	Q	R	Ι	L	R	L	F	H	V	Α	20
18	11	A	Т	Y	F	I	L	Ι	G	L	P	G	L	E	E	Α	19
19	54	E	H	S	L	Η	E	P	M	Y	Ι	F	\mathbf{L}	С	M	L	19
20	106	I	Н	S	L	S	G	М	E	s	T	V	\mathbf{L}	L	A	M	19
21	165	I	K	Q	L	P	F	C	R	S	N	Ι	\mathbf{L}	S	Η	S	19
22	191	С	D	D	I	R	v	И	V	v	Y	G	L	I	V	I	19
23	203	I	V	Ι	Ι	S	A	Ι	\mathbf{G}	L	D	S	L	L	Ι	S	19
24	213	S	L	L	I	S	F	S	Y	L	L	Ι	L	K	Т	V	19
25	224	L	K	Т	V	L	G	L	Т	R	E	A	Q	А	K	Α	19
26	227	V	L	G	L	Т	R	E	Α	Q	A	K	A	F	G	Т	19
27	248	A	V	F	I	F	Y	V	P	F	Ι	G	\mathbf{L}	S	M	V	19
28	254	v	P	F	I	G	L	S	M	v	H	R	F	S	K	R	19
29	277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	Ι	19

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HLA-DRB1*0301 (DR17) 15-mers

(SEQ ID NOS 2596-2671, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
30	36	L	Y	L	I	Α	v	L	G	N	L	Т	Ι	Ι	Y	I	18
31	93	T	Ι	Q	F	D	Α	C	L	L	Q	Ι	F	Α	Ι	Н	18
32	98	A	C	L	L	Q	I	F	Α	I	Н	S	L	s	G	M	18
33	125	Y	V	Α	I	С	н	Ρ	L	R	Н	Α	\mathbf{T}	v	\mathbf{L}	Т	18
34	158	M	Α	Р	L	Р	v	F	Ι	ĸ	Q	L	Р	F	C	R	18
35	187	M	K	L	A	С	D	D	Ι	R	V	N	V	V	Y	G	18
36	217	s	F	S	Y	L	L	I	L	ĸ	Т	V	${f L}$	G	\mathbf{L}	\mathbf{T}	18
37	225	ĸ	\mathbf{T}	V	L	G	L	\mathbf{T}	R	E	Α	Q	Α	K	Α	F	18
38	281	Y	L	\mathbf{L}	v	P	P	V	L	N	Р	I	V	Y	G	V	18
39	288	L	N	P	I	V	Y	G	V	ĸ	Т	K	\mathbf{E}	Ι	\mathbf{R}	Q	18
40	18	G	L	P	G	\mathbf{L}	E	E	Α	Q	F	W	L	Α	F	P	17
41	44	N	L	Т	I	I	Y	I	V	R	Т	E	Η	S	L	H	17
42	145	K	I	G	v	Α	Α	V	V	R	G	A	A	\mathbf{L}	М	Α	17
43	159	Α	Р	L	P	V	F	I	K	Q	L	P	F	C	R	S	17
44	256	F	Ι	G	L	S	M	V	Н	R	F	S	K	R	R	D	17
45	259	L	S	М	V	Н	R	F	S	K	R	R	D	S	P	L	17
46	137	v	L	\mathbf{T}	L	P	R	V	Т	K	Ι	G	V	Α	Α	V	16
47	262	v	Н	R	F	S	K	R	R	D	S	P	L	Р	V	Ι	16
48	294	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	F	16
49	46	T	Ι	I	Y	I	V	R	\mathbf{T}	E	Н	S	L	H	Е	Р	15
50	51	v	R	\mathbf{T}	E	Η	S	L	H	E	Р	M	Y	I	F	L	15
51	172	R	S	N	I	L	S	Η	S	Y	С	L	Н	Q	D	V	15
52	189	Ŀ	A	С	D	D	Ι	R	V	N	V	V	Y	G	L	Ι	15
53	212	D	S	L	L	1	S	F	S	Y	L	L	Ι	L	K	Т	15
54	218	F	S	Y	L	L	I	L	K	T	V	L	G	L	Т	R	15
55	271	S	P	L	P	V	Ι	L	Α	И	Ι	Y	L	L	V	P	15
56	279	N	I	Y	L	L	v	P	P	v	L	N	P	Ι	V	Y	15
57	12	T	Y	F	I	L	I	G	L	P	G	L	E	Ε	A	Q	14
58	35	s	L	Y	L	I	A	V	L	G	N	L	Т	Ι	I	Y	14
59	64	F	L	С	M	L	S	G	Ι	D	Ι	L	Ι	S	Т	S	14
60	140	L	Р	R	V	Т	K	Ι	G	V	A	A	V	V	R	G	14
61	273	L	P	V	Ι	L	A	N	I	Y	L	L	V	P	P	V	14
62	301	R	Q	R	I	L	R	L	F	H	V	A	T	Н	A	S	14
63	13	Y	F	I	L	Ι	G -	Г	P	G	L	Ε	E	A	Q	F	13
64	47	I	I	Y	I	V	R	T	E	H	S	Ь	Н	E	P	M	13
65	71	I	D	Ι	L	I	S	T	S	S	M	P	K	M	L	A	13
66	80	M	P	K	M	L	A	Ι	F	W	F	N	S	T	Т	I	13
67	109	L	S	G	M	E	S	T	V	L	L	A	M	A	F	D	13
68	113	E	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	13
69	135	A	Т	V	L	Т	L	P	R	V	Т	K	I	G	V		13
70	195	R	V	N	V	V	Y	G	L	Ι	V	I	Ι	S	A	I	13
71	202	L	I	V	I	Ι	S	A	I	G	L	D	S	L	L	I	13
72	220	Y	L	L	I	L	K	T	V	L	G	L	Т	R	E	A	13
73	221	L	L	Ι	L	K		V	L	G	L	T	R	E	A	Q	13
74	264	R	F	S	K	R	R	D	S	P	L	P	V	I	L	A	13
75	280	I	Y	L	L	V		P	V	L	N	P	I	V	Y	G	13
76	302	Q	R	1	L	R	L	F	Н	V	A	Т	H	Α	S	E	13

HLA-DRB1*0401 (DR4Dw4) 15-mers (SEQ ID NOS 2672-2805, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	36	L	Y	L	I	A	v	L	G	N	L	Т	I	I	Y	I	26
2	45	L	т	I	I	Y	I	v	R	т	E	Н	s	L	Н	E	26
3	68	L	s	G	I	D	I	L	Ι	s	Т	s	s	М	Р	ĸ	26
4	83	M	L	A	I	F	W	F	N	s	Т	т	I	Q	F	D	26
5	134	н	A	Т	v	L	т	L	P	R	V	т	K	ī	G	v	26
6	145	ĸ	I	G	v	A	A	v	v	R	G	Α	Α	L	М	Α	26
7	224	L	K	Т	v	L	G	L	Т	R	E	А	0	Α	ĸ	Α	26
8	227	v	L	G	L	T	R	E	Α	Q	Α	K	Ā	F	G	т	26
9	256	F	I	G	L	S	М	v	Н	R	F	s	ĸ	R	R	D	26
10	281	Y	L	L	v	Р	P	v	L	N	Р	Ι	V	Y	G	v	26
11	289	N	P	Ι	v	Y	G	v	K	т	K	Е	Ι	R	Q	R	26
12	301	R	0	R	I	L	R	L	F	н	v	Α	т	H	Ã	s	26
13	11	Α	T	Y	F	I	L	I	G	L	P	G	L	E	E	Α	22
14	24	E	Α	Q	F	W	L	A	F	P	L	C	s	L	Y	L	22
15	25	A	Q	F	W	L	A	F	P	L	С	s	L	Y	L	Ι	22
16	34	C	ŝ	L	Y	L	I	A	V	L	G	N	L	т	I	Ι	22
17	84	L	A	I	F	W	F	N	s	T	т	I	0	F	D	A	22
18	122	F	D	R	Y	V	A	I	C	н	P	L	R	Н	A	Т	22
19	197	N	v	V	Y	G	L	I	V	r	Ι	s	Α	I	G	L	22
20	215	L	I	s	F	s	Y	L	L	I	L	K	Т	v	L	G	22
21	217	s	F	s	Y	L	L	I	L	ĸ	Т	V	L	G	L	T	22
22	250	F	I	F	Y	v	P	F	I	G	L	s	М	V	Н	R	22
23	278	A	N	I	Y	L	L	v	P	P	v	L	N	P	I	V	22
24	19	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	L	20
25	30	A	F	P	L	С	s	L	Ŷ	L	Ι	Α	v	L	G	N	20
26	33	L	C	S	L	Y	L	I	Α	v	L	G	N	L	т	I	20
27	35	s	L	Y	L	I	A	v	L	G	N	L	Т	I	I	Y	20
28	39	I	A	v	L	G	N	L	Т	I	Ι	Y	Ι	v	R	Т	20
29	42	L	G	N	L	т	I	I	Y	I	V	R	т	E	Н	s	20
30	44	N	L	Т	I	I	Y	I	V	R	Т	Е	Н	s	\mathbf{L}	Н	20
31	48	I	Y	Ι	v	R	T	E	Н	s	L	Н	E	Р	М	Y	20
32	58	н	E	Р	м	Y	I	F	L	C	М	L	s	G	I	D	20
33	62	Y	I	F	L	С	M	L	s	G	Ι	D	1	L	Ι	S	20
34	65	L	С	М	L	S	G	I	D	I	L	I	S	Т	s	s	20
35	71	I	D	I	L	I	s	т	S	s	M	Ρ	K	М	L	Α	20
36	80	M	P	K	M	L	A	I	F	W	F	N	s	Т	\mathbf{T}	Ι	20
37	81	P	K	М	L	Α	I	F	W	F	N	s	Т	Т	Ι	Q	20
38	91	s	Т	Т	I	Q	F	D	Α	C	L	L	Q	I	F	Α	20
39	97	D	Α	С	L	L	Q	I	F	Α	I	Н	s	L	s	G	20
40	98	A	С	L	L	Q	I	F	Α	I	Н	s	L	s	G	М	20
41	100	L	L	Q	I	F	A	I	Н	s	L	S	G	М	E	s	20
42	103	I	F	Α	I	Н	S	L	s	G	М	E	S	Т	V	L	20
43	106	I	Н	S	L	S	G	М	Е	S	Т	V	L	L	A	М	20
44	115	T	V	L	L	Α		A	F	D	R	Y	V	Α	I	С	20
45	117	L	L	Α	M	Α	F	D	R	Y	V	Α	I	C	Н	Р	20
46		Y	V	A	I	С	н	P	L	R	Н	A	Т	V	L	Т	20
47		C	Н	P	L	R	Н	A	Т	v	L	\mathbf{T}	Ь	P	R	V	20
48		v		Т	L	Р	R	v	Т	ĸ	Ι	G	V	Α	Α	V	20
49		L	P	R	v	Т	K	I	G	v	A	A	V	V		G	20
														8	38		
														`	-		

HLA-DRB1*0401 (DR4Dw4) 15-mers (SEQ ID NOS 2672-2805, respectively in order of appearance)

	Pos	1			_	_	_	-	_	_			_	_		_	score
50	155	1 A	2 A	3 L	4	5	6	7	8	9	0	1	2	3	4	5	2.0
51			V	F	M	A	P	L	Þ	V	F	I	K	Q	L	P	20
52	162	P			I	K	Q	L	P	F	C	R	S	N	I	L	20
	165	I	K	Q	L	P	F	C	R	S	N	Ι	L	S	Н	S	20
53 54	179	S	Y	C	L	Н	Q	D	V	M	K	L	A	C	D	D	20
	183	H	Q	D	V	M	K	L	A	C	D	D	Ι	R	V	N	20
55	186	V	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	20
56	193	D	I	R	v	N	V	v -	Y	G	L	I	V	Ι	I	S	20
57	196	V	N	V	٧	Y	G	L	I	V	Ι	I	S	A	I	G	20
58	199	v	Y	G	L	Ι	V -	I	Ι	S	A	I	G	L	D	S	20
59	200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	20
60	202	L	I	V	I	Ι	S	A -	I	G	L	D	S	Г	L	I	20
61	203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	20
62	206	I	S	A	I	G	L	D	S	L	L	I	S	F	S	Y	20
63	208	A.	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	20
64	211	L	D	S	L	L	I	S	F	S	Y	L	L	Ι	L	K	20
65	212	D	S	L	L	I	S -	F	S	Y	L	L	Ι	L	K	Т	20
66	218	F	S	Y	L	L	I	L	K	T	V	L	G	L	Т	R	20
67	240	G	Т	C	V	S	н	V	С	A	V	F	Ι	F	Y	V	20
68	243	V	S	Н	v	C	A	V	F	I	F	Y	V	Р	F	Ι	20
69	246	V	C	A	V	F	Ι	F	Y	V	Р	F	Ι	G	L	S	20
70	248	A	V	F	I	F	Y	V	Р	F	I	G	L	S	М	V	20
71	251	I	F	Y	V	Р	F	Ι	G	L	s	M	V	H	R	F	20
72	272	P	L	Р	V	Ι	L	Α	N	I	Y	L	L	V	Р	Р	20
73	277	L	Α	N	Ι	Y	L	L	V	P	P	V	L	N	P	Ι	20
74	285	P	Р	V	L	N	P	Ι	V	Y	G	V	K	Т	K	E	20
75	18	G	L	Р	G	L	E	E	A	Q	F	W	L	Α	F	P	18
76	27	F	W	L	Α	F	P	L	C	s	L	Y	L	Ι	Α	V	18
77	69	S	G	Ι	D	Ι	L	I	s	T	S	S	M	P	K	M	18
78	94	Ι	Q	F	D	A	С	ь	L	Q	Ι	F	A	Ι	Н	S	18
79	99	С	L	L	Q	Ι	F	A	Ι	Н	S	L	S	G	M	Ε	18
80	107	H	S	Ь	S	G	M	Е	s	T	V	L	L	Α	M	A	18
81	116	v	L	L	A	M	A	F	D	R	Y	V	A	Ι	C	Н	18
82	126	V	A	Ι	С	H	P	L	R	H	A	\mathbf{T}	V	L	Т	L	18
83	164	F	Ι	K	Q	L	P	F	С	R	S	N	Ι	L	S	Н	18
84	176	L	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	18
85	187	M	K	L	A	С	D	D	Ι	R	V	И	V	V	Y	G	18
86	205	I	Ι	S	A	Ι	G	L	D	S	L	L	Ι	S	F	S	18
87	233	E	Α	Q	A	K	A	F	G	T	С	V	S	Η	V	С	18
88	237	K	A	F	G	\mathbf{T}	С	V	Ş	Н	V	C	Α	V	F	Ι	18
89	271	S	Р	L	P	V	Ι	L		N	Ι	Y	L		V	Р	18
90	293	Y	G	V	K	\mathbf{T}	K	E	I	R	Q	R	Ι	L	R	L	18
91	294	G	V	K	т	K	Е	I	R	Q	R	I	Ļ	R	L	F	18
92	10	S	A	Т	Y	F	I	L	Ι	G	L	P	G	L	Ε	Ε	16
93	28	W	L	A	F	P	L	C	S	L	Y	L	Ι	A	V	L	16
94	59	E	P	M	Y	Ι	F	L	С	M	L	S	G	Ι	D	Ι	16
95	61	M	Y	Ι	F	L	C	M	L	s	G	I	D	I	L	Ι	16
96	85	A	Ι	F	W	F	N	S	Т	T	1	Q	F	D	A	С	16
97	101	L	Q	Ι	F	A	I	H	S	L	S	G	M	E	S	T	16
98	177	S	H	S	Y	С	ŗ	H	Q	D	V	M	K	L		С	16
														8	9		

HLA-DRB1*0401 (DR4Dw4) 15-mers (SEQ ID NOS 2672-2805, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
99	236	A	K	A	F	G	T	ď	V	s	Н	V	C	A	V	F	16
100	249	v	F	I	F	Y	v	P	F	I	G	L	s	M	V	Н	16
101	253	Y	V	P	F	Ī	G	L	S	M	V	Н	R	F	s	K	16
102	13	Y	F	I	L	I	G	L	P	G	L	E	E	Ā	Q	F	14
103	14	F	I	L	I	G	L	P	G	L	E	E	A	0	F	W	14
104	16	L	I	G	L	P	G	L	E	E	A	0	F	W	L	A	14
105	38	L	1	Α	v	L	G	N	L	т	r	ī	Y	1	v	R	14
106	47	I	Ι	Y	I	V	R	T	E	н	s	L	Н	E	Р	М	14
107	54	E	Н	s	L	Н	E	P	М	Y	I	F	L	С	М	L	14
108	60	P	М	Y	I	F	L	C	М	L	s	G	I	D	I	L	14
109	64	F	L	С	M	L	s	G	I	D	Ι	L	Ι	s	\mathbf{T}	s	14
110	70	G	I	D	I	L	I	s	Т	s	s	М	P	K	М	L	14
111	72	D	1	L	I	S	T	s	S	M	Ρ	K	М	\mathbf{L}	Α	Ι	14
112	109	L	S	G	M	E	s	T	V	L	L	Α	M	Α	F	D	14
113	113	E	S	\mathbf{T}	V	L	L	Α	М	A	F	D	R	Y	V	Α	14
114	135	A	\mathbf{T}	V	L	Т	L	P	R	v	т	K	I	G	V	Α	14
115	143	v	Т	K	I	G	v	A	Α	v	V	R	G	Α	Α	L	14
116	148	V	Ą	Α	v	V	R	G	Α	A	L	М	Α	P	L	P	14
117	149	Α	Α	V	v	R	G	A	Α	L	М	Α	P	L	P	V	14
118	154	G	Α	A	L	М	A	P	L	P	V	F	Ι	K	Q	L	14
119	158	M	Α	Р	L	P	v	F	I	K	Q	L	P	F	C	R	14
120	173	S	N	I	L	S	H	S	Y	C	L	Н	Q	D	V	M	14
121	184	Q	D	V	M	K	L	Α	C	D	D	Ι	R	V	N	V	14
122	191	С	D	D	I	R	V	N	V	v	Y	G	L	Ι	V	Ι	14
123	195	R	V	N	v	V	Y	G	L	I	V	Ι	Ι	S	A	Ι	14.
124	213	s	L	\mathbf{L}	I	S	F	S	Y	L	L	Ι	\mathbf{L}	K	\mathbf{T}	V	14
125	220	Y	L	L	I	L	K	T	V	L	G	L	Т	R	E	Α	14
126	221	L	L	Ι	L	K	Т	v	L	G	L	Т	R	E	A	Q	14
127	225	K	Т	V	L	G	L	Т	R	E	A	Q	A	K	A	F	14
128	259	L	S	M	V	H	R	F	S	K	R	R	D	S	Р	L	14
129	270	D	S	Р	L	Р	v	Ι	L	Α	N	Ι	Y	Ĺ	L	V	14
130	273	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	14
131	274	P	V	I	L	A	И	I	Y	L	L	V	P	Ρ	V	L	14
132	280	I	Y	L	L	V	P	P	V	L	N	P	Ι	V	Y	G	14
133	284	V	Þ	P	V	L	N -	P	1	v	Y	G	V	K	T	K	14
134	302	Q	R	Ι	L	R	L	F	Н	V	A	Т	H	A	S	E	14

HLA-DRB1*1101 15-mers

(SEQ ID NOS 2806-2866, respectively in order of appearance)

	Pos .																score
		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	BCCIC
1	145	K	I	G	v	Α	A	V	V	R	G	Α	Α	L	М	A	28
2	122	F	D	R	Y	V	A	I	C	Н	P	L	R	Н	Α	Т	25
3	217	S	F	s	Y	L	L	I	L	K	Т	V	L	G	L	Т	25
4	197	N	V	V	Y	G	L	I	V	I	Ι	S	Α	I	G	\mathbf{L}	24
5	10	s	Α	\mathbf{T}	Y	F	I	L	I	G	L	P	G	L	E	E	23
6	255	P	F	Ι	G	L	s	М	V	H	R	F	s	K	R	R	23
7	44	N	L	\mathbf{T}	I	I	Y	I	V	R	\mathbf{T}	\mathbf{E}	Н	S	L	Н	22
														9	00		

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively
in order of appearance)

_	Pos									_	_	_	_	_		_	score
		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	22
8	59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	22
9	158	M	A	P	L	P	V	F	Ι	K	Q	L	P	F	C F	R I	22
10	237	K	A	F	G	T	C	V	S	H	V	C	A	V			
11	74	L	Ι	Ş	T	S -	S	M	P	K	M	L	A	I	F	W	21
12	134	Н	A	T	V	L	T -	L	P	R	V	T	K	I	G	V	20
13	137	V	L	Т	L	P	R	V	T	K	I	G	V	A	A	V	20
14	162	P	V	F	I	K	Q	L	P	F	C	R	S	N	Ι	L	20
15	199	V	Y	G	L	Ι	V	I	I	S	A	Ι	G	L	D	S	20
16	224	L	K	T	V	L	G	L	Т	R	Ε	A	Q	A	K	A	20
17	256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	20
18	290	P	Ι	V	Y	G	v	K	Т	K	E	Ι	R	Q	R	I	20
19	301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	20
20	65	L	С	M	ь	S	G	I	D	I	L	I	S	T	S	S	19
21	100	L	L	Q	I	F	A	Ι	Н	S	L	S	G	M	E	S	19
22	196	V	И	V	V	Y	G	L	Ι	V	Ι	I	S	A	I	G	19
23	218	F	S	Y	L	L	Ι	L	K	T	V	L	G	L	T	R	19
24	247	C	A	V	F	1	F	Y	V	P	F	I	G	L	S	M	19
25	274	P	V	Ι	L	A	N	Ι	Y	L	L	V	P	P	V	Ь	19
26	45	L	Т	Ι	I	Y	I	V	R	T	E	H	S	L	H	E	18
27	68	L	S	G	I	D	Ι	L	I	S	Т	S	S	M	P	K	18
28	80	M	P	K	M	\mathbf{L}	Α	I	F	W	F	N	S	T	T	I	18
29	97	D	A	C	L	L	Q	1	F	A	Ι	Н	S	Ь	S	G	18
30	103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	18
31	208	A	I	G	L	D	S	L	Ļ	I	S	F	S	Y	L	L	18
32	249	V	F	Ι	F	Y	v	P	F	Ι	G	L	S	M	V	H	18
33	61	M		Ι	F	\mathbf{L}	C	M	L	S	G	Ι	D	Ţ	L	I	17
34	215	L	I	S	F	S	Y	L	L	I	L	K	Т	V	L	G	17
35	259	L	S	M	V	Н	R	F	S	K	R	R	D	S	P	L	17
36	278	A		I	Y	L	L	V	P	P	V	L	N	Þ	Ι	V	17
37	288	L	N	Р	I	V	Y	G	V	K		K		I	R	Q	17
38	11	A		Y	F	Ι	L	I	G	L	P	G		Ε	E	A	16
39	24	E	A	_	F	W	L	A	F	P	L			L	Y	L	16
40	42	L			L	Т	I	I	Y	I				Ε	H		16
41	253	Y			F	Ι	G	L	S	M					S	K	16
42	47	I				V	R	Т	E	H					P	M	15
43	99	С				Ι	F	A		H				G			15
44	116	V					A	F	D	R					C		15
45	143	V				G	V	A									15
46	179	S				H	Q		V								15
47					L) A						15
48		S															15
49		M															15
50		I															15
51		P															15
52		S															14
53		Y															14
54		V															14
55		I															14
56	170	F	, ,	: R	S	N	Ι	L	S	H	I S	; Y	? C		. E	[Q	14
															91		

HLA-DRB1*1101 15-mers (SEQ ID NOS 2806-2866, respectively in order of appearance)

	Pos																score
		1.	2	3	4	5	6	7	8	9	0	1	2	3	4	5	
57	180	Y	С	L	H	Q	D	V	М	ĸ	\mathbf{L}	Α	C	D	D	I	14
58	193	D	I	R	v	N	v	V	Y	G	L	Ι	V	I	Ι	S	14
59	229	G	L	Т	R	E	A	Q	Α	K	Α	F	G	T	С	V	14
60	270	D	S	P	L	P	v	I	L	A	N	I	Y	L	L	V	14
61	298	ĸ	E	I	R	Q	R	I	L	R	\mathbf{L}	F	Н	V	Α	T	14

Table XXIX, beginning at page 213, line 1, has been amended as follows:

Table XXIX. Nucleotide sequence in the 5' region close to 101P3A11 gene (SEQ ID NO: 2867).

<i>!</i> •						
						TTCACCATGT
61	TGGCCTGGCT	GGTCTCGAAC	CCCTGACCTT	GCGATCTGCC	CACCTCGGCC	TCCCAAAGTG
121	CTGGGATTAC	AGGCGTGAGC	CACTGTACCT	GGCGGGGCTT	ATTGTTTTTT	AAAAAGATTT
181	CCAAAACCTT	GCCCTGGCAA	TTCTGATTTT	CTGGGCCTGG	AGCAGGACCT	GGAGGGATGG
241	TGTTGTCAAT	TACTTTAGAT	GTTTCTATCA	GGAAAGTTTG	AGAAATGGTA	TTCAGGCCTA
301	AACACAAACC	TCTCTTGAAA	TCTCATCCCA	GACTGAGCCC	CTGCTCCCTA	TCTTAAATTA
361	GATTATAGTA	GGTCTTAAAG	TCAGCTGTAG	ACTGAGCCTC	TAAATCTGAA	CCCAGACCCA
	CCCTAACCCC					
481	AAGTCTACTC	${\tt TGATGGGAAA}$	AGGCTAAGAG	CAGTGCCCTG	GGCAGCAACA	TCAGCTCTGA
541	AGATGCAGGA	${\tt CTGTGTTACA}$	${\tt TGTTTTATGA}$	GTGGGTCTTC	ACACACTGAG	ATTCATGGGA
601	CAGTAATAGA	ATCTGCTTGT	GCAGCACTGG	GGCCTTGGAG	GGTCAGGGTA	AGGCTCAAGA
	TGTCCAGGAA					
721	CAGGATGACT	${\tt TAGTCCTGTT}$	TGTTACTGTC	ACCACTCCAA	TGCCTTTTCC	TCATTAGTCC
781	TTTCTCTCCT	${\tt CTGAGCCACA}$	ACTAAATGAT	${\tt GTTTCTACTT}$	TTCCCTTTCT	ACTTTCCTAG
841	ACCCTGGATT	${\tt TTGTATGCAG}$	AAGCCCCAGC	TCTTGGTCCC	TATCATAGCC	ACTTCAAATG
	GAAATCTGGT					
961	TACACTTTTG	GCTGGCTTTC	CCACTGTGTT	TTATGTATGC	CTTGGCCACC	CTGGGTAACC
	TGACCATTGT					
1081	TGGCCATGCT	TTCCACTATT	GACCTAGTCC	TCTCCTCTAT	CACCATGCCC	AAGATGGCCA
1141	GTCTTTTCCT	GATGGGCATC	CAGGAGATCG	AGTTCAACAT	TTGCCTGGCC	CAGATGTTCC
1201	TTATCCATGC	TCTGTCAGCC	GTGGAGTCAG	CTGTCCTGCT	GGCCATGGCT	TTTGACCGCT
	TTGTGGCCAT					
1321	AGATTGGACT	ATCTGCCCTG	ACCAGGGGGT	TTGTATTCTT	CTTCCCACTG	CCCTTCATCC
1381	TCAAGTGGTT	GTCCTACTGC	CAAACACATA	CTGTCACACA	CTCCTTCTGT	CTGCACCAAG
1441	ATATTATGAA	GCTGTCCTGT	ACTGACACCA	GGGTCAATGT	GGTTTATGGA	CTCTTCATCA
	TCCTCTCAGT					
1561	GGGCTGTTTT	GGAGCTGTCC	TCTCGGAGGG	CAGCACTCAA	GGCTTTCAAC	ACCTGCATCT
1621	CCCACCTCTG	TGCTGTTCTG	GTCTTCTATG	TACCCCTCAT	TGGGCTCTCG	GTGGTGCATA
1681	GGCTGGGTGG	TCCCACCTCC	CTCCTCCATG	TGGTTATGGC	TAATACCTAC	TTGCTGCTAC
1741	CACCTGTAGT	CAACCCCCTT	GTCTATGGAG	CCAAGACCAA	AGAGATCTGT	TCAAGGGTCC
	TCTGTATGTT					
1861	ACAGAAGATG	GGAATATTAG	GATCCTATTG	AATGCCTTGG	TGATTAAAGT	ATCAAACCTA
1921	TTGTGCTGTC	TTCTTCCAGC	AATTTAAGTA	GATCATGTAT	TCTGTCTCCA	GGAATGTGTC
1981	AGTACTGAAC	TTATGACCCT	GTCTGGACAT	CCTGGAGAAT	GACTGCACTA	GTCCCTCTGC
2041	TATGGTGGTC	TTGCCTTCTC	CTTCTCTCTC	AGCTAGAAAA	TACATCTAGT	TTTGACATGG
2101	GGAGGCTGTA	AAGATCACAC	CTCATGGTTC	ATTCCAGTTT	TGAAGTATGA	TTTTAATGTT

2161	CTTGCCCCCA	TGTGCCCATG	TTGGTGAATT	TGCATGGACT	ATAAACGTTA	TTGCAAATAC
					GTATTTGGGG	
2281	GGAGAGACAG	CAACAAGACA	AGAGGCAGCT	CACATGCAAT	GTTGAAGTTT	CTGTATGCAA
2341	GAGGGTGTGT	TGGCAGATTT	GTGAAATCTG	CCCATTTGCA	TCTGTATGGC	TCTATATGAC
					TGAATGTGTG	
2461	TGTGGACACT	TGCTTTTCAG	TGTGCGTATA	TGTGAGAGAG	AGGGTGCACA	CATGGAATAC
2521	GTACTGGTTG	TGTCCTGGTG	AGTGTGGTAG	CTATGTCCTG	GCACATGTAT	GTTTCATGAG
					${\tt TTAGTTGGTA}$	
2641	GTCTACGTGA	GAATGCTGGT	${\tt GTCTGTATCT}$	$\tt GCATGGTGGG$	CAGTACCTTT	ATGTGTATCT
2701	GGTAAGAATG	CTGCCTCTAC	${\tt CTTTTCTTCC}$	${\tt TATTTGTACT}$	ATGTGAATGT	GGTGCATGAA
					ATCTTTCAGC	
2821	GTATGTCCAC	TGTGCATAAT	ATTTGAGATG	TAAAACCATT	${\tt TTGTGCGGTA}$	TATGTGTTAT
2881	TAGTTGTAAG	TCGGTGAAAT	GTACATCTGA	ATTCTGTGTG	CATATTGTTG	GTACTGATGC
2941	TATTTTCGTG	CATATGTCTA	GTGTATATGT	${\tt TTTAAGGCAA}$	ACTTTCTTTG	TGTGTTGGGT
3001	GTGTATGTGA	CACGAATGGG	GACAGCATCT	${\tt GTATTTCTGA}$	$\tt GCATGGATTG$	ATGTGTGGTG
3061	TCTGTATGTA	TCTTGGAATG	GAGGAGGAG	ATTGAAGAAG	TCTGGCTGTG	AGCAGCAGAA
3121	ATAATTTCCA	AAGTTGAGTG	ACATGACTCT	AAGATGCCCA	GTTTCTCGGC	CTGGGGTCAG
3181	CCTGGGTGAT	AGCTCAGTCT	GTCAGAATGA	AAGGAAACAC	GGTGCTTCCT	TGCTCCACCT
3241	TTTCACAGGC	CAGACCACAC	CTTCTTCATC	CTGAACACAA	${\tt GGATTTCAAG}$	GGCTTTTGTT
3301	ACCTCTTCCT	ACGTTTCCTG	CCTCTGCTAT	CCGAGGCACT	GGCCTCCCTA	AACCCTGCCC
3361	TCCTGCCTCA	ATAGCAAGTC	ATGGTATCCT	CACCTCTCCC	TTCCCTTTTT	GGCTTATCT
3421	CCAAACATGT	ATAAAAGTCC	TTGGTTCCCC	ATCTCTACTA	AAAATACAAC	AATTAGCCGG
3481	GTGTGATGGC	GCGTGCCTGT	AGTCCCAGCT	AGTTGGGAGG	CTGAGGCAGG	AGAAACGCTT
3541	GAGCCCGCAA	GGTGGAGGTT	GCAGTGAGCC	GAGATCATGC	CACTGCACTC	CAGCCTGGTG
3601	ACAGAGCAAG	ACTCTGTGTC	AAAAAAAAA	AAAAAAAAA	AGCCTTGGTT	GTAGGGAGTT
3661	TCTCCTAATC	CCTCTGGGAA	AGCAAGGGTG	GAGGGGAAGC	CAGTCAATCT	CCCTTCTGTT
					TGTAGCATTC	
					TTGTTACTCC	
					TGTCTAAGTT	
3901	ATGGAGGCAG	CAGAGATGGC	TCCAGGGTTC	TGATAGCAAG	TGTCAGGCTG	CGTGCTCTGT
3961	AGGCACCAGA	AACTGTTGTC	ACCAGTAATT	TTGATGTGGT	CTGAGTTAGA	ATGGTCTGAT
					TGTGTTCTGA	
					AACTAAAAAC	
					TATTTAGTTT	
4201	TTGTTCTCTA	ACTCTCTAAA	ATGTTCTCTG	ACTATTTTTG	CCCTTAAGGG	AGAAACCAGA
					GTTAAAGAAA	
4321	TGTCCTCAGC	CAGAAGTTCA	GTAATCCAAG	GCCAGAGAGT	GGACGGCAGA	GGCACTGTCC
4381	CTGGGGACCT	TGGTTATAAG	TTATCCAGAC	ACAGGGACCA	GAGCCTGGGA	GACAAAAAAA
					GTGAATTCCA	
					GAAAGAACAC	
					TCCTTTGCCA	
					TCACGAAGAC	
					CCTTCACATT	
					TCCCTTTCCC	
					GCTGAGAAGC	
					GGACAGCATT	
					AATAAATAAC	
4981	GAGGTCCAAG	GGAGTAGGCG	GAG Acagaga	ggctgtattt	cagtgcagcc	tgccagacct

Note: The three high score predictions of promoters were bold and underlined. The lower case sequence indicates the beginning part of the transcript of 101P3A11 gene.

Table XXX, beginning at page 214, line 35, has been amended as follows

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Table XXX: Promoters and their positions predicted by Neural Network Promoter Prediction computer program (various portions of SEQ ID NO: 2867, respectively, in order of appearance).

Start	End	Score	Promoter Sequence
25	75	0.91	TTTTGCATTTTTAATAGAGGCAGGGTTTCACCATGTTGGCCTGGCTGG
665	715	0.95	CAGGAAGTTGTATATAAGGAGAATCAGAGCAGAGAGAGACTAGGGTTCAG
2477	2527	0.91	TCAGTGTGCGTATATGTGAGAGAGAGGGTGCACACATGGAATACGTACTG
3139	3189	0.82	TGACATGACTCTAAGATGCCCAGTTTCTCGGCCTGGGGTCAGCCTGGGTG
3420	3470	0.96	GCCAAACATGTATAAAAGTCCTTGGTTCCCCATCTCTACTAAAAATACAA
4092	4142	0.99	AACTGATCAGTAAAAAATAAGGGGAGACCAACTAAAAACCATGTTGTTCT
4953	5003	0.97	AGGCAGAGAATAAATAACCCTGACCAGGGAGGTCCAAGGGAGTAGGCGGA

Table XXXI, beginning at page 215, line 1, has been amended as follows:

Table XXXI: Alignment of five homologous 5' upstream genomic regulatory regions of the human 101P3A11 and PSA genes.

Query: 5' upstream regulatory region of the PSA gene Subject: Putative 5' upstream regulatory region of the 101P3A11 gene.

Nucleic acid sequences predicted to be binding sites for the indicated transcription factors are **bolded**, <u>underlined</u>, or *italicized*.

1.	NF-1 SP-1 NF-1
Query: 3864	ccaggctggagtgcagtggcagtctcggctcactgcaacctctgcctcccaggttcaa 3923
(SEQ ID NO:	
·	
Shict: 3598	ccaggctggagtgcagtggcatgatctcggctcactgcaacctccaccttgcgggctcaa 3539
(SEQ ID NO:	
TODO ID NO.	20097
000000 2024	gtgattctcctgcctcagcctcctgagttgctgggattacaggcatgcagcaccatgccc 3983
Query: 3924	
01-1-1 2520	
SDJCL: 3538	gcgtttctcctgcctcagcctcccaactagctgggactacaggcacgcgccatcacaccc 3479
Query: 3984	agctaatttttgtatttttagtagagatgggg 4015
Sbjct: 3478	ggctaattgttgtatttttagtagagatgggg 3447
2.	
	cctgtaatcccagctactgaggaggctgaggcaggagaatcacttgaacccagaaggcag 4729
(SEQ ID NO:	
(528 25 110)	
Chict. 2406	cctgtagtcccagctagttgggaggctgaggcaggagaaacgcttgagcccgcaaggtgg 3555
(SEQ ID NO:	
(SEQ ID NO:	SP1 NF-E
	
4530	
Query: 4730	aggttgcaatgagccgagattgcgccactgcactccagcctgggtgacagagtgagactc 4789
Sbjct: 3556	aggttgcagtgagccgagatcat gcca c <i>tgcac</i> tccagcct-ggtgacagagcaagactc 3614
Query: 4790	tgtctcaaaaaaaaaaa 4807

Sbjct: 3615 tgtgtcaaaaaaaaaaa 3632

3.
GR NF-1 SP1
Query: 142 tgagactgagtctcgctctgtgcccaggctggagtgcagtggtgcaaccttggctcactg 201
(SEQ ID NO: 2872)
Sbjct: 3621 tgacacagagtcttgctctgtcaccaggctggagtgcagtggcatgatctcggctcactg 3562
(SEQ ID NO: 2873)
Query: 202 caageteegeeteetgggtteacgecatteteetgeeteageeteetgagtagetgggae 261
Sbjct: 3561 caacetecacettgegggeteaagegttteteetgeeteageeteecaaetagetgggae 3502
DDJCC. 3501 caaccccacacccagagaccaaagagaccaagaccaagaccaagaccaagaccaagacaagacaagacaagacaagacaagacaagacaagacaagac
NF-1
Query: 262 tacaggcacccgccaccacgcctggctaannnnnnngtatttttagtagagatgggg 318
Sbjct: 3501 tacaggcacgcgcatcacacccggctaattgttgtatttttagtagagatgggg 3447
4.
Query: 300 atttttagtagagatggggtttcactgtgttagccaggatggtctcagtctcctgacctc 359
(SEQ ID NO: 2874)
Sbjct: 31 atttttaatagaggcagggtttcaccatgttggcctggctgg
(SEQ ID NO: 2875)
<u>NF-1</u>
LF-A1 CP2
Query: 360 gtgatctgccaccttggcctcccaaagtgctgggattacaggcgtgagccactgcgcct 419
Sbjct: 91 gcgat <i>ctgccc</i> acctcggcctcccaaagtgctgggattacaggcgtga gccact gtacc t 150
NF-1
Query: 420 ggc 422
Sbjct: 151 ggc 153
5.
NF-1
NF-1 CP2
Query: 4506 gccaggcacagtggctcacgcctgtaatcccaacaccatgggaggctgagatgggtggat 4569
(SEQ ID NO: 2876)
Sbjct: 153 gccaggtacagtggctcacgcctgtaatcccagcactttgggaggccgaggtgggcagat 94
(SEQ ID NO: 2877)
Query: 4566 cacgaggtcaggagtttgagaccagcctgaccaacatggtgaaactctgtctcta 4620
Sbjct: 93 cgcaaggtcaggggttcgagaccagccaggccaacatggtgaaaccctgcctcta 39

x /

Figure 1 (SEQ ID NO:2878)

FIG. 2A (SEQ ID NOS:2879 & 2880)

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	51	as a	303	9	mcm.	እመመ	18			27				Cara					54 TGG
	5.																		
		ACA	AAG	63 GGG		ACA	72 CAT			81 CAT		GTT			CTA				108 TGC
*				117			126			135			144			153			162
												GAT						TCC	
										M		D							s
				171			180			189			198			207			216
		GCT	ACA		TTC	ATC			GGC	CTC	CCT	GGT	TTA	GAA	GAG	GCT	CAG	TTC	TGG
		 A	T	Y	F	ī	L	I				G					Q		w
				225			234			243			252			261			270
		TTG	GCC		CCA	TTG			CTC			ATT			CTA		AAC	TTG	
		 T.		 F	 P	 T.									 L	 G	 N		 T
		-	••		•	_		_	_			_			_			_	
		ATC	ATC	279 TAC	ATT	GTG	288 CGG	ACT	GAG	297 CAC		CTG	306 CAT		CCC	315 ATG		ATA	324 TTT
				-5-															
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		СТТ	TGC	333 ATG	СТТ	TCA	342 GGC	ATT	GAC	351 ATC		ATC	360 TCC		TCA	369 TCC		ccc	378 AAA
		L	C	M	L	s	G	Ι	D	I	L	I	S	T	S	s	М	P	ĸ
				387			396			405			414			423	<i>0</i> .0m	mam	432
		ATG	CTG		ATC							ACC				GAT			
		M	L	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	C	L
				441			450			459			468			477			486
				ATT		GCC	ATC	CAC	TCC	TTA	TCT	GGC	ATG				GTG		
		L	Q	I	P	A	I	н	s	L	s	G	M	B	s	T	. V	L	L
*				495			504			513			522			531			540
		GCC	ATG	GCT	TTT	GAC	CGC	TAT	GTG	GCC	ATC	TGT	CAC	CCA	CTG	CGC	CAT	GCC	ACA
		A	M	A	F	D	R	Y	v	A	I	C	H	P	L	R	H	A	. т
				549			558			567			576			585			594
		GTA	CTT	ACG	TTG				ACC	AAA	ATT	GGT	GTG	GCT	GCT	GTG	GTG	CGG	GGG
		v	r L	T	L	P	R	v	T	ĸ	I	G	v	A	A	v	v	R	G
				603			612			621			630			639			648
		GCT	GCA				CCC			GTC	TTC	ATC	AAG	CAG		CCC			CGC
		 A	 A																
		-	-				-		-	•	_	_		-		_		_	

FIG. 2B

		657			666			675			684			693			702
mcc	ידיאא	ATC	CTTT	TCC	CAT	TCC	TAC	TGC	CTA	CAC	CAA	GAT	GTC	ATG	AAG	CTG	GCC
100	MAI	AIC	C11	100													
							17	C	L	H	Q	D	v	м	ĸ	L	A
S	N	I	L	S	H	5	I	C	ь	Д	¥	D	•	14		_	•
		711			720			729			738			747			756
тст	GAT	GAT	ATC	CGG	GTC	AAT	GTC	GTC	TAT	GGC	CTT	ATC	GTC	ATC	ATC	TCC	GCC
				ъ	v	NT	17	v	v	G	т.	I	v	I	I	S	A
C	D	D	-	K	٧	14	٧	•	-	·	~		•	_	_	-	
														001			810
		765			774			783			792			801			
ATT	GGC	CTG	GAC	TCA	CTT	CTC	ATC	TCC	TTC	TCA	TAT	CTG	CTT	ATT	CTT	AAG	ACT
т.	G	L	D	S	L	L	I	s	F	S	Y	L	L	I	L	ĸ	T
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					828			837			846			855			864
		819			040				~~~	330		marar	ccc		TCC	GTC	
GTG	TTG	GGC	TTG	ACA	CGT	GAA	GCC		GCC	AAG		111	GGC	ACI	100	GIC	101
v	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	C	v	s
•																	
		873			882			891			900			909			918
		TGT	a am	ama	mma	3773	THE C		CTA	CCT		ATT	GGA	TTG	TCC	ATG	GTG
CAT	GTG	TGT	GCT	GIG		MIM	110		GIA								
																37	37
H	v	C	A	v	F	I	F	Y	V	₽	F	I	G	L	S	M	v
		927			936			945			954			963			972
an m	aca	TTT	NGC.	AAG	CGG	ССТ	GAC	TCT	CCG	CTG	CCC	GTC	ATC	TTG	GCC	AAT	ATC
CAT	CGC	111	AGC	AAG													
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		981			990			999			1008			1017			1026
		981			990			999			1008			1017			
TAT	CTG	981 CTG			990			999		ATT	1008	TAT		1017			
TAT	CTG	981 CTG	GTT	CCT	990 CCT	GTG	CTC	999 AAC	CCA	ATT	1008 GTC	TAT	GGA	1017 GTG	AAG	ACA	AAG
TAT	CTG	981 CTG	GTT		990 CCT		CTC	999 AAC	CCA	ATT	1008 GTC	TAT	GGA	1017 GTG	AAG		AAG
TAT	CTG	981 CTG	GTT	CCT P	990 CCT P	GTG V	CTC L	999 AAC N	CCA P	ATT	1008 GTC V	TAT Y	GGA G	1017 GTG V	AAG K	ACA T	AAG K
TAT Y	CTG L	981 CTG L	GTT V	CCT P	990 CCT P	GTG V	CTC L	999 AAC N 1053	CCA P	ATT	1008 GTC V 1062	TAT Y	GGA G	1017 GTG V 1071	AAG K	ACA T	AAG K 1080
TAT Y	CTG L	981 CTG L	GTT V	CCT P	990 CCT P	GTG V	CTC L	999 AAC N 1053	CCA P	ATT	1008 GTC V 1062	TAT Y	GGA G	1017 GTG V 1071	AAG K	ACA T	AAG K 1080 GAG
TAT Y	CTG L	981 CTG L	GTT V	CCT P	990 CCT P	GTG V	CTC L CGA	999 AAC N 1053	CCA P TTC	ATT I CAT	1008 GTC V 1062	TAT Y GCC	GGA G	1017 GTG V 1071	AAG K	ACA T	AAG K
TAT Y GAG	CTG L ATT	981 CTG L 1035 CGA	GTT V CAG	CCT P	990 CCT P 1044 ATC	GTG V	CTC L CGA	999 AAC N 1053 -CTT	CCA P	ATT	1008 GTC V 1062 GTG	TAT Y GCC	GGA G	1017 GTG V 1071 CAC	AAG K	ACA T	AAG K 1080 GAG
TAT Y	CTG L	981 CTG L 1035 CGA	GTT V	CCT P	990 CCT P 1044 ATC	GTG V	CTC L CGA	999 AAC N 1053	CCA P	ATT I CAT	1008 GTC V 1062 GTG	TAT Y GCC	GGA G G	1017 GTG V 1071 CAC	AAG K GCT	ACA T	AAG K 1080 GAG
TAT Y GAG	CTG	981 CTG L 1035 CGA	GTT V CAG	CCT P CGC	990 CCT P 1044 ATC	GTG V CTT	CTC L CGA	999 AAC N 1053 CTT L	CCA P TTC	ATT I CAT	1008 GTC V 1062 GTG	TAT Y GCC	GGA G ACA	1017 GTG V 1071 CAC	AAG K GCT	ACA T TCA	AAG K 1080 GAG E
TAT Y GAG	CTG	981 CTG L 1035 CGA	GTT V CAG	CCT P CGC	990 CCT P 1044 ATC I	GTG V CTT	CTC L CGA	999 AAC N 1053 -CTT L	CCA P TTC	ATT I CAT	1008 GTC V 1062 GTG V	TAT Y GCC	GGA G ACA	1017 GTG V 1071 CAC H	AAG K GCT	ACA T TCA	AAG K 1080 GAG E
TAT Y GAG	CTG L ATT	981 CTG L 1035 CGA R	GTT V CAG	CCT P CGC R	990 CCT P 1044 ATC I	GTG V CTT L	CTC L CGA	999 AAC N 1053 -CTT L	CCA P TTC	ATT I CAT	1008 GTC V 1062 GTG V	TAT Y GCC A	GGA G ACA T	1017 GTG V 1071 CAC H	AAG K GCT A	ACA T TCA S	AAG K 1080 GAG E 1134
TAT Y GAG	CTG L ATT	981 CTG L 1035 CGA	GTT V CAG	CCT P CGC R	990 CCT P 1044 ATC I	GTG V CTT L	CTC L CGA	999 AAC N 1053 -CTT L	CCA P TTC	ATT I CAT	1008 GTC V 1062 GTG V	TAT Y GCC A	GGA G ACA T	1017 GTG V 1071 CAC H	AAG K GCT A	ACA T TCA S	AAG K 1080 GAG E
TAT Y GAG	CTG L ATT	981 CTG L 1035 CGA R	GTT V CAG	CCT P CGC R	990 CCT P 1044 ATC I	GTG V CTT L	CTC L CGA	999 AAC N 1053 -CTT L	CCA P TTC	ATT I CAT	1008 GTC V 1062 GTG V	TAT Y GCC A	GGA G ACA T	1017 GTG V 1071 CAC H	AAG K GCT A	ACA T TCA S	AAG K 1080 GAG E 1134
TAT Y GAG	CTG L ATT I	981 CTG L 1035 CGA R	GTT V CAG	CCT P CGC R	990 CCT P 1044 ATC I	GTG V CTT L	CTC L CGA	999 AAC N 1053 -CTT L	CCA P TTC	ATT I CAT	1008 GTC V 1062 GTG V	TAT Y GCC A	GGA G ACA T	1017 GTG V 1071 CAC H	AAG K GCT A	ACA T TCA S	AAG K 1080 GAG E 1134
TAT Y GAG	CTG L ATT I	981 CTG L 1035 CGA R	GTT V CAG	CGC P CGC R	990 CCT P 1044 ATC I 1098	GTG V CTT L	CTC L CGA	999 AAC N 1053 L 1107	CCA P TTC	CAT	1008 GTC V 1062 GTG V 1116	GCC	GGA G ACA T TCC	1017 GTG V 1071 CAC H	AAG K GCT A GAT	ACA T TCA	AAG K 1080 GAG E 1134
TAT Y GAG	CTG L ATT	981 CTG L 1035 CGA R 1089	GTT V CAG Q	CCT P CGC	990 CCT P 1044 ATC I 1098 ATC	GTG V CTT L	CTC L CGA R	999 AAC N 1053 CTT L 1107 CTT	CCA P TTC	CAT	1008 GTC V 1062 GTG V 1116	TAT Y GCC	GGA G ACA T T	1017 GTG V 1071 CAC H 1125	AAG K GCT A GAT	ACA T TCA S	AAG K 1080 GAG E 1134 GAT 1188
TAT Y GAG	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG	GTT V CAG Q	CCT P CGC R GTG	990 CCT P 1044 ATC I 1098 ATC	GTG V CTT L	CTC L CGA R CTT	999 AAC N 1053 -CTT L 1107	CCA P TTC	CAT H CAT	1008 GTC V 1062 GTG V 1116 TCA	TAT Y GCC A GAG	GGA G ACA T T CC	1017 GTG V 1071 CAC H 1125 TCT	AAG K GCT A GAT	ACA T TCA S TCA	AAG K 1080 GAG E 1134 GAT 1188
TAT Y GAG E CCC	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG	CAG Q TCA	CGC P CGC R	990 CCT P 1044 ATC I 1098 ATC	GTG V CTT L	CTC L CGA R CTT	999 AAC N 1053 -CTT L 1107 	CCA P TTC	CAT H CAT	1008 GTC V 1062 GTG V 1116 TCA	GCC A GAG	GGA G ACA T TCC	1017 GTG V 1071 CAC H 1125 TCT	AAG K GCT A GAT	ACA T TCA S	AAG K 1080 GAG E 1134 GAT 1188 AAA
TAT Y GAG E CCC	L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG	GTT V CAG	CCT P CGC R	990 CCT P 1044 ATC I 1098 ATC 	GTG V CTT L	CTC L CGA R CTT	999 AAC N 1053 CTT L 1107 CTT 	CCA TTC F TTC	CAT H CAT	1008 GTC V 1062 GTG V 1116 TCA 	TAT Y GCC A GAG	GGA G ACA T TCCC	1017 GTG V 1071 CAC H 1125 TCT 	AAG K GCT A GAT	ACA T TCA S TCA	AAG K 1080 GAG E 1134 GAT 1188 AAA 1242
TAT Y GAG CCC P	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG	GTT V CAG Q TCA	CCT P CGC R GTG	990 CCT P 1044 ATC I 1098 ATC 1152	GTG V CTT L AAA	CTC L CGA R CTT	999 AAC N 1053 CTT L 1107 CTT 	CCA P TTC F TTC	CAT CAT CAT CAT CAT	1008 GTC V 1062 GTG V 1116 TCA 	GCC A GAG	GGA G ACA T T CCC	1017 GTG V 1071 CAC H 1125 TCT 	AAG GCT A GAT	ACA T TCA S TCA	AAG K 1080 GAG E 1134 GAT 1188 AAA 1242
TAT Y GAG CCC P	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG	GTT V CAG	CCT P CGC R GTG	990 CCT P 1044 ATC I 1098 ATC 1152	GTG V CTT L AAA	CTC L CGA R CTT	999 AAC N 1053 CTT L 1107 CTT 	CCA P TTC F TTC	CAT CAT CAT CAT CAT	1008 GTC V 1062 GTG V 1116 TCA 	GCC A GAG	GGA G ACA T T CCC	1017 GTG V 1071 CAC H 1125 TCT 	AAG GCT A GAT	ACA T TCA S TCA	AAG K 1080 GAG E 1134 GAT 1188 AAA 1242
TAT Y GAG CCC P	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG 1143 GTT	GTT V CAG	CCT P CGC R GTG	990 CCT P 1044 ATC I 1098 ATC 1152 TTG 	GTG V CTT L AAA	CTC L CGA R CTT	999 AAC N 1053 CTT L 1107 CTT 	CCA P TTC	CAT CAT CAT CAT CAT	1008 GTC V 1062 GTG V 1116 TCA 1224 GTT	GCC A GAG	GGA ACA T TCCC	1017 GTG V 1071 CAC H 1125 TCT 1233 TCT	AAG GCT A GAT CTT	ACA T TCA S TCA	AAG K 1080 GAG E 1134 GAT 1188 AAA 1242
TAT Y GAG CCC P TTT AAAA	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG 1197	CAG Q TCA	CCT P CGC R GTG	990 CCT P 1044 ATC I 1098 ATC 1152 TTG 1260	GTG V CTT L AAA	CTC L CGA R CTT	999 AAC N 1053 -CTT L 1107 1161 1215 1269	CCA P TTC	CAT CAT CAT CAT	1008 GTC V 1062 GTG V 1116 TCA 1224 GTT 1278	GCC A GAG	GGA ACA T TCCC	1017 GTG V 1071 CAC H 1125 TCT 1233 TCT	AAG K GCT A GAT CTT CCA	ACA T TCA S TCA TCA TTA	AAG K 1080 GAG E 1134 GAT 1188 AAA 1242 TTT 1296
TAT Y GAG CCC P TTT AAA	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG 1197 CAAC	GTT V CAG	CCT P CGC R GTG	990 CCT P 1044 ATC I 1098 ATC 1206 CCT	GTG V CTT L AAA	CTC L CGA R CTT	999 AAC N 1053 CTT L 1107 CTT 1269	CCA P TTC F TTC	CAT CAT CAT CAT CAT CAG	1008 GTC V 1062 GTG V 1116 TCA 1224 GTT 1278	GCC A GAG	GGA ACA T T TCC	1017 GTG V 1071 CAC H 1125 TCT 1233 TCT	AAG K GCT A GAT CCA TAC	ACA T TCA S TCA S TCA S CCCT	AAG K 1080 GAG E 1134 GAT 1188 AAA 1242 TTT 1296
TAT Y GAG CCC P TTT AAA	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG 1197 CAAC	GTT V CAG	CCT P CGC R GTG	990 CCT P 1044 ATC I 1098 ATC 1206 CCT	GTG V CTT L AAA	CTC L CGA R CTT	999 AAC N 1053 CTT L 1161 AGT 1215 ATG 1215	CCA P TTC F TTC	CAT CAT CAT CAT CAT CAG	1008 GTC V 1062 GTG V 1116 TCA 1224 GTT 1278	GCC A GAG	GGAA T TCCC	1017 GTG V 1071 CAC H 1125 TCT 1233 TCT	AAG GCT A GAT CCA TAC	ACA T TCA S TCA TCA TTA	AAG K 1080 GAG E 1134 GAT 1242 TTT 1296
TAT Y GAG CCC P TTT AAA	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG 1197 AAC	GTT V CAG	CCT P CGC R GTG	990 CCT P 1044 ATC I 1098 ATC 1206 CCT	GTG V CTT L AAA	CTC L CGA R CTT	999 AAC N 1053 CTT L 1161 AGT 1215 ATG 1215	CCA P TTC F TTC	CAT CAT CAT CAT CAT CAG	1008 GTC V 1062 GTG V 1116 TCA 1224 GTT 1278	GCC A GAG	GGAA T TCCC	1017 GTG V 1071 CAC H 1125 TCT 1233 TCT	AAG GCT A GAT CCA TAC	ACA T TCA S TCA TCA TTA	AAG K 1080 GAG E 1134 GAT 1188 AAA 1242 TTT 1296
GAG GAG CCC P TTT AAAA	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG 1197 AAC	GTT V CAG	CCT P CGC R GTG	990 CCT P 1044 ATC I 1098 ATC 1206 CCT 1260 CTT	GTG V CTT L AAA	CTC L CGA R CTT A GAC	999 AAC N 1053 CTT L 1107 CTT 1215 ATG 1215 ATG 1269	CCA P TTC F TTC	CAT	1008 GTC V 1062 GTG V 1116 TCA 1278 GTT 1278	GCC A GAG	GGAA T TCCC	1017 GTG V 1071 CAC H 1125 TCT 1233 TCT 1287	AAG K GCT A GAT CCA TAC	ACA T TCA S TCA S TCA S CCCT	AAG K 1080 GAG E 1134 GAT 1188 AAA 1242 TTT 1296 GAC 1350
GAG GAG CCC P TTT AAAA	CTG	981 CTG L 1035 CGA R 1089 GTG 1143 GTT 1197 AAC	GTT V CAG	CGT P CGC R GTG	990 CCT P 1044 ATC I 1098 ATC 1206 CCT 1260 CCT 1314 A GGG	GTG V CTT L AAA	CTC L CGA R CTT A TTT	999 AAC N 1053 CTT L 1107 CTT 1269 CTT 1323	CCA P TTC F TTC ATT	CAT	1008 GTC V 1062 GTG V 1116 TCA 1224 GTT 1278 TAT	GCC A GAG GAG AAA CCA	GGAA T TCCC GAA TAT	1017 GTG V 1071 CAC H 1125 TCT 1233 TCT 1287 TAA	AAG K GCT A GAT CCA TAC	ACA T TCA S TCA S TCA S CCT CCT AAAT	AAG K 1080 GAG E 1134 GAT 1242 TTT 1296

FIG. 2C

				206	1205	-	1404
1359 AAC TGC TTC	1368	1377		.386 	בככב	ממת שמש	
AAC TGC TTC	TAC TGA TGG	TTT ACA	GCA TTC	TGA GAT	AAG AAI	GGI ACA	ICI AGA
1412	1422		421	1440		1449	1458
1413	CCA AAG GCC	T CC2	CCC C	7770	מת מתת	ACA GAA	דאר דאד
GAA CAT TIG	CCA AAG GCC	IAA GCA		AGG ALL			
1467	1476	1	485	1494		1503	1512
1407	TAN TCT AGC	מממ מידים	מד מיים	CTT CCT	CTT CAG	AAC TCC	CAA CCA
AAA AIG AGA		IIA AAA					
1521	1530	1	539	1548		1557	1566
CAT TGG ATC	TCA GAA AAA	TGC TGT	CTT CAA	AAT GAC	TTC TAC	AGA GAA	GAA ATA
1575	1584	1	.593	1602		1611	1620
ልጥጥ ጥጥጥ ሮርጥ	CTG GAC ACT	AGC ACT	TAA GGG	GAA GAT	TGG AAG	TAA AGC	CTT GAA
1629	1638	1	647	1656		1665	1674
AAC ACT ACA	TTT ACC TAC	GTT AAT	GAA AGT	TGA CAC	ACT GTT	CTG AGA	GTT TTC
1683	1692	1	701	1710		1719	1728
ACA GCA TAT	GGA CCC TGT	TTT TCC	TAT TTA	ATT TTC	TTA TCA	ACC CTT	TAA TTA
							
1737	1746	1	1755	1764		1773	1782
GGC AAA GAT	ATT ATT AGT	ACC CTC	ATT GTA	GCC ATG	GGA AAA	TTG ATG	TTC AGT
1791	1800	. 1	L809	1818		1827	1836
GGG GAT CAG	TGA ATT AAA	TGG GGT	CAT ACA	AGT ATA	AAA ATT	AAA AAA	AAA AAA
1845	1854	. 1	L863	1872		1881	1890
CAC TTC ATG	CCC AAT CTC	ATA TGA	TGT GGA	AGA ACT	GTT AGA	GAG ACC	AAC AGG
						 -	
1899			L9 1 7	1926		1935	1944
GTA GTG GGT	TAG AGA TTT	CCA GAG	TCT TAC	ATT TTC	TAG AGG	AGG TAT	TTA ATT
. 1953		. 1	L971	1980		1989	1998
ጥርጥ ጥርጥ ር ልር	TCA TCC AGT	GTT GTA	TTT AGG	AAT TTC	CTG GC	ACA GAA	CTC ATG
2007	2016		2025	2034		2043	2052
CCT TTA ATC	CCA CTA GCT	ATT GCT	TAT TGT	CCT GGT	CCA ATT	GCC AAT	TAC CTG
						 -	
2061			2079	2088		2097	2106
שכיר כידי המא	AGA AGT GAT	TTC TAG	GTT CAC	CAT TAT	GGA AGA	TTC TTA	TTC AGA
2115			2133	2142		2151	2160
አአር ጥርጥ ርርል	TAG GGC TT	TAG CAA	GTT ATT	TAT TTT	TAA AAG	TTC CAT	AGG TGA
ANG ICI GCA						- -	
2169			2187	2196		2205	2214
שבע שבע שבע	GCA GTG AGG	TTA GGG	AGC CAC	CAG TTA	TGA TG	GAA GTA	TGG AAT
IIC ION INC						-	
222	2232	•	2241	2250		2259	2268
4443 CCC 3CC TCT	TGA AGA TA	- \ CAT TGG	CCT TTT	GAG TGT	GAC TC	TAG CTG	GAA AGT
GGC NGG ICI	. IGA AGA IA						
222	2280		2295	2304		2313	2322
44//	TTC AGG ACC	, ግ አጥር፤ ርጥጥ	ጥልጥ ጥጥር	GGG CTT	TGT GC		
GAG GGA ATC	TIC AGG ACC	AIG CII					
	2340		2349	2358		2367	2376
2331	ACC AGG AA	מרש שתר	TG7 CUU	ልሮርኒ ሮልጥ	GGG AA'		
GAC TTT GAG	ACC AGG AA	a GCM MIC	IGA CII	.100. CAI			
					_		

FIG. 2D

	2205		2204		2403	٠,	2412		2421		2420
СТТ											ATA TGA
	2439		2448		245	7	2466		2475		2484
CAA	CAG TGT	TAA	CCA AGA	AAC	TCA AA	TAC	AAA TAC	TAA	AAC ATG	TGA	TCA TAT
	2493										2538
ATG	TGG TAA	GTT	TCA TTT	TCT	TTT TO	A ATC	CTC AGG	TTC	CCT GAT	ATG	GAT TCC
	2547		2556		256		2574		2502		2592
ייי אייי											GCC TAT
171	AAC AIG						0A1 A1C				GCC TAI
	2601						2628	•	2637		2646
TTA											TAT TAT
	2655						2682				2700
TGA	ATG TCA	TCT									TCC CCC
							0036				
3.00	2709										2754 TTT CAT
AGC	AAA GIG						100 110				III CAI
	2763										2808
CAA	ACC TGA					_					
	2817										2862
TTG	AGT TGG	GTA	TTA TTA								AAG TGA
											2916
CAT	GTG CAA						ACC CTC			GCC	TTT CAT
	2925										2970
GTT	GAC ATT					-					
	2979		2988	•	299	7	3006		3015		3024
AAG	CCT GGA	TTT	CTG AAA	AAA	CTG TG	C AGA	GCC AAA	CCT	CTG TCA	TTT	GCA ACT
	3033										3078
CCC	ACT TGT	ATT	TGT ACG	AGG	CAG TI	G GAT	AAG TGA		ATA AAG		TAT TGT
	2007		2006		210	 5	2114				3132
GTC											AAA AAA

AAA A 3'

Figure 3: Protein Sequence for 101P3A11 (piece of SEQ ID NO:2880)

MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDILI STSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHATVLTLPRVTKIGV AAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYL LILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYG VKTKEIRQRILRLFHVATHASEP

Figure 4

Query: 330 AMKKL 334 (SEQ ID NO:2881) + +L Sbjct: 303 RILRL 307 (SEQ ID NO:2882)

Alignme	ent o	of 101P3A11 (Sbjct) with mouse olfactory receptor S25 (Query)	
Query:	34	GNYTVVTEFILLGLTDDITVSVILFVMFLIVYSVTLMGNLNIIVLIRTSPQLHTPMYLFL GN + T FIL+GL L +Y + ++GNL II ++RT LH PMY+FL	93
Sbjct:	6	GNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL	65
Query:	94	SHLAFLDIGYSSSVTPIMLRGFLRKGTFIPVAGCVAQLCIVVAFGTSESFLLASMAYDRY L+ +DI S+S P ML F T I C+ Q+ + + ES +L +MA+DRY	153
Sbjct:	66	THE PROPERTY OF THE PROPERTY O	125
Query:	154	VAICSPLLYSTQMSSTVCILLVGTSYLGGWVNAWIFTGCSLNLSFCGPNKINHFFCDYSP VAIC PL ++T ++ + + + G L FC N ++H +C +	213
Sbjct:	126	VAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQD	185
_		LLKLSCSHDFSFEVIPAISSGSIIVVTVFIIALSYVYILVSILKMRSTEGRQKAFSTCTS ++KL+C V I S I + +I+ SY+ IL ++L + + E + KAF TC S	
Sbjct:	186	VMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS	244
		HLTAVTLFFGTITFIYVMPQSSYSTDQNKVVSVFYTVVIPMLNPLIYSFRNKEVKE H+ AV +F+ + FI + +S ++ +++ Y +V P+LNP++Y + KE+++	
Sbjct:	245	HVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQ	302

Figure 23: Alignment of 101P3A11-PHOR-1 with the rat GPCR RA1C (gi|3420759).

Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%)

- PHOR: 14 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73 F+LIG+PGLEEA FW FPL S+Y +A+ GN +++IVRTE SLH PMY+FLCML+ ID+
- RAIC: 11 FMLIGIPGLEEAHFWFGFPLLSMYAVALFGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70
- PHOR: 74 LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133 +STS+MPK+LA+FWF+S I FDACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
- RAIC: 71 ALSTSTMPKILALFWFDSREITFDACLAQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130
- PHOR: 134 HATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193 HA VL +IG+ A+VRG+ PLP+ IK+L FC SN+LSHSYC+HQDVMKLA D
- RAIC: 131 HAAVLNNTVTVQIGMVALVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYTD 190
- PHOR: 194 IRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
- NVVYGL I+ +G+D + IS SY LI++ VL L ++ +AKAFGTCVSH+ V F RA1C: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRAVLQLPSKSERAKAFGTCVSHIGVVLAF 250
- PHOR: 253 YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311 (SEQ ID NO:2883)
 YVP IGLS+VHRF D + V++ ++YLL+PPV+NPI+YG KTK+IR R+L +F ++
- RAIC: 251 YVPLIGLSVVHRFGNSLDPIVHVLMGDVYLLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309 (SEQ ID NO:2884)

Figure 24: Alignment of 101P3A11-PHOR-1 with the human prostate specific GPCR. (gi | 13540539)

Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%)

- PHOR: 14 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73 F+LIG+PGLE+A FW+ FPL S+Y++A+ GN +++IVRTE SLH PMY+FLCML+ ID+
- GPCR: 11 FVLIGIPGLEKAHFWVGFPLLSMYVVAMFGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70
- PHOR: 74 LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
- +STS+MPK+LA+FWF+S I F+ACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR GPCR: 71 ALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130
- PHOR: 134 HATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
 HA VL +IG+ AVVRG+ PLP+ IK+L FC SN+LSHSYC+HQDVMKLA D
- GPCR: 131 HAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYAD 190
- PHOR: 194 IRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252 NVVYGL I+ +G+D + IS SY LI++TVL L ++ +AKAFGTCVSH+ V F
- GPCR: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAF 250
- PHOR: 253 YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311(SEQ ID NO:2885)
 YVP IGLS+VHRF + V++ +IYLL+PPV+NPI+YG KTK+IR R+L +F ++
- GPCR: 251 YVPLIGLSVVHRFGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309 (SEQ ID NO:2886)

Figure 25: Alignment with human olfactory receptor 5II12 (gi]14423836)

Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%)

- PHOR: 7 NESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLC 66 N + +F+L G+PGLE + WL+ PLC +Y +A+ GN I+ VR E SLHEPMY FL
- HOR5: 5 NVTHPAFFLLTGIPGLESSHSWLSGPLCVMYAVALGGNTVILQAVRVEPSLHEPMYYFLS 64
- PHOR: 67 MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126 MLS D+ IS +++P +L F N+ I FDACL+Q+F IH S MES +LLAM+FDRYV
- HOR5: 65 MLSFSDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYV 124
- PHOR: 127 AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 186
 AIC PLR+ATVLT + +G+ A R + PLP IK+LP CRSN+LSHSYCLH D+
- HOR5: 125 AICDPLRYATVLTTEVIAAMGLGAAARSFITLFPLPFLIKRLPICRSNVLSHSYCLHPDM 184
- PHOR: 187 MKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH 245
 M+LAC DI +N +YGL V++S G+D I SY+LIL++V+ +RE + KA TCVSH
- HOR5: 185 MRLACADISINSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSH 244
- PHOR: 246 VCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRIL 305
- + AV FYVP IG+S VHRF K + V+++N+YL VPPVLNP++Y KTKEIR+ I HOR5: 245 ILAVLAFYVPMIGVSTVHRFGKHVPCYIHVLMSNVYLFVPPVLNPLIYSAKTKEIRRAIF 304
- PHOR: 306 RLFH 309 (SEQ ID NO:2887)

R+FH

HOR5: 305 RMFH 308 (SEQ ID NO:2888)

Figure 1 (SEQ TO NO: 2878)

FIG. 2A (SEQ TO MOS: 1879 \$ 2880)

5 '	as a	3.C3	9	m/m	איייי	18					אמא			CTC.	45	GAA	GNC	54 TCC
ο.																		
			63			72			81					C/m x	99		maa	108
																GCC	TGG	TGC
	maa	max.	117		200		mmC.		1		CAT			aaa	153		TCC	162
			CAG					_			GAI					GAA		
								M	M	v	D	P	N	G	N	E	s	s
			171			180			189			198			207			216
	GCT	ACA			ATC							-				CAG	TTC	
	A	T	¥	F	1	L	I	G	ь	P	G	ъ	E	E	A	Q	P	W
			225															
	TTG	GCC	TTC	CCA	TTG	TGC	TCC	CTC	TAC	CTT	ATT	GCT	GTG	CTA	GGT	AAC	TTG	ACA
	L	A	F	P	L	С	s	L	Y	L	I	A	v	L	G	N	L	T
									0.05			200			215			224
	ATC	ATC	279	ATT	GTG	288 CGG		GAG		AGC		306 CAT		ccc	315 ATG	TAT	ATA	
	I	I	¥	I	v	R	T	E	н	S	L	H	E	P	M	Y	I	F
			333			342			351			360			369			378
	CTT	TGC	ATG	CTT	TCA	GGC	ATT				ATC	TCC	ACC	TCA	TCC	ATG	CCC	
	 L		м	 L	 s	 G		 D		 L		s	т	s	s	M	 P	
		_	11		3	G	-	Ď	-	-	_		•	_		••	•	20
			387			396									423			432
	ATG	CTG	GCC	ATC	TTC	TGG	TTC	AAT	TCC	ACT	ACC	ATC	CAG	TTT	GAT	GCT	TGT	CTG
	M	L	A	I	F	W	F	N	s	T	T	I	Q	F	D	A	C	L
			441			450			459			468			477			486
	CTA	CAG		TTT	GCC									TCC		GTG	CTG	
	L	Q	I	F	A	I	н	S	ь	S	G	M	B	S	T	. v	L	L
			495			504						522			531			540
	GCC	ATG	GCT	TTT	GAC	CGC	TAT	GTG	GCC	ATC	TGT	CAC	CCA	CTG	CGC	CAT	GCC	ACA
	A	M	A	F	D	R	Y	v	A	I	c	н	P	L	R	н	A	T
	CTA	Caba.	549	ייים אינים ייים אינים	CCT		CTC		567		CCT	576 GTG		CCT	585 GTG	GTG	cee	594 GGG
	v	L	T	L	P	R	v	T	K	I	G	v	A	A	v	v	R	G
			603			612			621			630			639			648
	GCT	GCA		ATG	GCA											TTC		
																 F		
	Δ	Α.	1.	M	Α.	2	L.		v				U	- 14	~	r.	•	ĸ

FIG. 2B

		657			666			675	1 1		684			693			702
mcc	222	ATC	CTT	TCC	CAT	TCC	TAC	TGC	CTA	CAC	CAA	GAT	GTC	ATG	AAG	CTG	GCC
TCC	WWI	AIC	CII	100													
								C		7.7	Q	ъ	v	M	ĸ	L	A
S	И	I	L	s	H	S	Y	C	ъ	n	Q	D	٧	1.7			
		711			720			729			738			747			
m/Cm	CAT	GAT	ATC	CGG	GTC	AAT	GTC	GTC	TAT	GGC	CTT	ATC	GTC	ATC	ATC	TCC	GCC
161	GAI	GAI	AIC														
										~	τ.	I.	v	I	I	s	A
С	D	D	I	R	V	N	V	٧	1	G		• .	•	_	_	-	
		765			774			783			792			801			810
ידידע	GGC	CTG	GAC	TCA	CTT	CTC	ATC	TCC	TTC	TCA	TAT	CTG	CTT	ATT	CTT	AAG	ACT
A	000																
								s			v	L	L	I	L	ĸ	т
I	G	L	D	5	71	ш	_		-	_	-	_	_	-	_		_
														055			864
		819			828			837			846			855			
GTG	TTG	GGC	TTG	ACA	CGT	GAA	GCC	CAG	GCC	AAG	GCA	TTT	GGC	ACT	TGC	GTC	TCT
		G	L	T	R	B	A	Q	A	ĸ	A	F	G	T	С	v	S
v	L	G	н	-		13	•	×				_	_				
											000			909			918
		873			882			891			900						
CAT	GTG	TGT	GCT	GTG	TTC	ATA	TTC	TAT	GTA	CCT	TTC	ATT	GGA	TTG	TCC	ATG	GTG
н	v	С	A	v	F	I	F	Y	v	P	F	I	G	L	S	M	v
n	٧	•	•	•	-	_	_	_									
								045			954			963			972
		927			936			945									
CAT	CGC	TTT	AGC	AAG	CGG	CGT	GAC	TCT	CCG	CTG	CCC	GTC	ATC	TTG	GCC	AAT	ATC
	 D				5	 R							I	L	A	N	ī
н	R	 F	 s	к	3 .	R		s					I	L	A	N	I
н	R		_	ĸ	R	R		s	P	L	P	v					
		0.01	_		R 990	R	D	s 999	P	L	P 1008	v		1017			1026
		0.01	_		R 990	R	D	S 999 AAC	P CCA	L ATT	P 1008 GTC	V	GGA	1017			1026
		0.01	GTT	CCT	990 CCT	R GTG	D CTC	999 AAC	P CCA	L ATT	P 1008 GTC	V TAT	GGA	1017 GTG	AAG	ACA	1026 AAG
TAT	CTG	981 CTG	GTT	CCT	990 CCT	R GTG	D CTC	999 AAC	P CCA	L ATT	P 1008 GTC	V TAT	GGA	1017	AAG		1026 AAG
	CTG	981 CTG	GTT	CCT	990 CCT	R GTG	D CTC	S 999 AAC	P CCA	L ATT	P 1008 GTC	V TAT	GGA	1017 GTG	AAG	ACA	1026 AAG
TAT	CTG	981 CTG	GTT V	CCT P	990 CCT P	R GTG V	D CTC L	999 AAC N	P CCA P	L ATT	P 1008 GTC V	V TAT	GGA G	1017 GTG V	AAG K	ACA T	1026 AAG K
TAT	CTG L	981 CTG L	GTT V	CCT P	990 CCT P	R GTG V	D CTC L	999 AAC N	P CCA P	L ATT	P 1008 GTC V 1062	V TAT Y	GGA G	1017 GTG V	AAG K	ACA T	1026 AAG K 1080
TAT	CTG L	981 CTG L	GTT V	CCT P	P 990 CCT P 1044 ATC	GTG V	D CTC L	999 AAC N 1053	P CCA P	L ATT I	P 1008 GTC V V 1062 GTG	V TAT Y	GGA G G	1017 GTG V	AAG K	ACA T	1026 AAG K 1080 GAG
TAT Y GAG	CTG L	981 CTG L	V	P	990 CCT P 1044 ATC	GTG	CTC	999 AAC N 1053	P CCA P TTC	L ATT	P 1008 GTC V 1062 GTG	V TAT Y GCC	GGA G	1017 GTG V 1071 CAC	AAG	ACA T	1026 AAG K 1080 GAG
TAT Y GAG	CTG	981 CTG L 1035 CGA	GTT V CAG	P	990 CCT P 1044 ATC	GTG	CTC	999 AAC N 1053	P CCA P TTC	L ATT	P 1008 GTC V 1062 GTG	V TAT Y GCC	GGA G	1017 GTG V	AAG	ACA T	1026 AAG K 1080 GAG
TAT Y GAG	CTG	981 CTG L 1035 CGA	GTT V CAG	P	990 CCT P 1044 ATC	GTG	CTC	999 AAC N 1053	P CCA P TTC	L ATT I CAT	P 1008 GTC V 1062 GTG	V TAT Y GCC	GGA G ACA	1017 GTG V 1071 CAC H	AAG K GCT A	ACA T TCA	1026 AAG K 1080 GAG E
TAT Y GAG	CTG	981 CTG L 1035 CGA	GTT V CAG	CCT P CGC	990 CCT P 1044 ATC	GTG V CTT L	CTC	999 AAC N 1053 CTT	P CCA P TTC	L ATT I CAT	P 1008 GTC V 1062 GTG	V TAT Y GCC	GGA G ACA	1017 GTG V 1071 CAC H	AAG K GCT A	ACA T TCA	1026 AAG K 1080 GAG E
TAT Y GAG	CTG L ATT	981 CTG L 1035 CGA R	GTT V CAG	CGC P CGC	R 990 CCT P 1044 ATC I	GTG V CTT L	CTC	999 AAC N 1053 CTT L	P CCA P TTC	L ATT I CAT	P 1008 GTC V 1062 GTG V	V TAT Y GCC	GGA G ACA	1017 GTG V 1071 CAC H	AAG K GCT A	ACA T TCA	1026 AAG K 1080 GAG E
TAT Y GAG	CTG L ATT	981 CTG L 1035 CGA R	GTT V CAG	CGC P CGC	P 1044 ATC I 1098	R GTG V CTT L	D CTC	999 AAC N 1053 -CTT L	P CCA P TTC F	L ATT	P 1008 GTC V 1062 GTG V	V TAT Y GCC A	GGA G ACA T	1017 GTG V 1071 CAC H	AAG K GCT A	ACA T TCA	1026 AAG K 1080 GAG E
TAT Y GAG	CTG L ATT	981 CTG L 1035 CGA R	GTT V CAG	CGC P CGC	P 1044 ATC I 1098	R GTG V CTT L	D CTC	999 AAC N 1053 CTT L	P CCA P TTC F	L ATT	P 1008 GTC V 1062 GTG V	V TAT Y GCC A	GGA G ACA T	1017 GTG V 1071 CAC H	AAG K GCT A	ACA T TCA	1026 AAG K 1080 GAG E
GAG	CTG L ATT	981 CTG L 1035 CGA R	GTT V CAG	CGC P CGC	P 1044 ATC I 1098	R GTG V CTT L	D CTC	999 AAC N 1053 -CTT L	P CCA P TTC F	L ATT	P 1008 GTC V 1062 GTG V	V TAT Y GCC A	GGA G ACA T	1017 GTG V 1071 CAC H	AAG K GCT A	ACA T TCA	1026 AAG K 1080 GAG E
TAT Y GAG	CTG L ATT I	981 CTG L 1035 CGA R	GTT V CAG	CGC P CGC	P 1044 ATC I 1098	GTG V CTT L	CTC L CGA R CTT	999 AAC N 1053 CTT L 1107	P CCA TTC	L ATT	P 1008 GTC V 1062 GTG V	V TAT Y GCC A GAG	GGA G ACA T	1017 GTG V 1071 CAC H	AAG K GCT A	ACA T TCA	1026 AAG K 1080 GAG E 1134
GAG	CTG L ATT I	981 CTG L 1035 CGA R	CAG	CGC P CGC R	990 CCT P 1044 ATC I 1098	GTG V CTT L	CTC L CGA R CTT	999 AAC N 1053 CTT L 1107	P CCA TTC	L ATT	P 1008 GTC V 1062 GTG V	V TAT Y GCC A GAG	GGA G ACA T	1017 GTG V 1071 CAC H	AAG K GCT A	ACA T TCA	1026 AAG K 1080 GAG E 1134
GAG	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089	CAG	CCT P CGC	990 CCT P 1044 ATC I 1098 ATC	R GTG V CTT L	CTC L CGA	999 AAC N 1053 -CTT L 1107	P CCA P TTC	L ATT	P 1008 GTC V 1062 GTG V 1116	V TAT Y GCC A GAG	GGA G ACA T	1017 GTG V 1071 CAC H 1125	AAG K GCT A	TCA	1026 AAG K 1080 GAG E 1134 GAT
GAG	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089	CAG	CGC	P 990 CCT P 1044 ATC I 1098 ATC	R GTG V CTT L AAA	CTC L CGA R CTT	999 AAC N 1053 -CTT L 1107	P CCA P TTC	L ATT	P 1008 GTC V 1062 GTG V 1116 TCA	V TAT Y GCC A GAG	GGA G ACA T TCC	1017 GTG V 1071 CAC H 1125 TCT	AAG K GCT A GAT	ACA T TCA S TCA	1026 AAG K 1080 GAG E 1134 GAT
GAG	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG	CAG Q TCA	CGC R	990 CCT P 1044 ATC I 1098 ATC	GTG V CTT L	CTC L CGA R CTT	999 AAC N 1053 CTT L 1107 CTT	P CCA P TTC	L ATT	P 1008 GTC V 1062 GTG V 1116	TAT Y GCC A GAG	GGA G ACA T TCC	1017 GTG V 1071 CAC H 1125 TCT	AAG K GCT A GAT	ACA T TCA S TCA	1026 AAG
GAG CCC P	L ATT	981 CTG L 1035 CGA R 1089 GTG	CAG Q CAG	P CGC	990 CCT P 1044 ATC I 1098 ATC	GTG V CTT L	CTC L CGA R CTT	999 AAC N 1053 -CTT L 1107 1161 1215	P CCA TTC	L ATT	1008 GTC V 1062 GTG GTG V 1116 TCA	TAT Y GCC A GAG	GGA G ACA T T CC	1017 GTG V 1071 CAC H 1125 TCT 	AAG K GCT A GAT	ACA T TCA S TCA	1026 AAG
TAT Y GAG	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG	CAG Q GTT AAC	P CGC	990 CCT P 1044 ATC 1098 ATC	GTG V CTT L	CTC L CGA R CTT	999 AAC N 1053 -CTT L 1107 1161 AGT 1215	P CCA P TTC	L ATT I CAT H CAT	1008 GTC V 1062 GTG V 1116 TCA 	TAT Y GCC A GAG	GGA G ACA T TCC	1017 GTG V 1071 CAC H 1125 TCT 1179	AAG K GCT A GAT	ACA T TCA S TCA S TCA TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1026 AAG
TAT Y GAG	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG	CAG Q GTT AAC	P CGC	990 CCT P 1044 ATC 1098 ATC	GTG V CTT L	CTC L CGA R CTT	999 AAC N 1053 -CTT L 1107 1161 AGT 1215	P CCA P TTC	L ATT I CAT H CAT	1008 GTC V 1062 GTG V 1116 TCA 	TAT Y GCC A GAG	GGA G ACA T TCC	1017 GTG V 1071 CAC H 1125 TCT 1179	AAG K GCT A GAT	ACA T TCA S TCA S TCA TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1026 AAG
TAT Y GAG	CTG	981 CTG L 1035 CGA R 1089 GTG 	CAG Q GTT AAC	CCT P CGC R	990 CCT P 1044 ATC 1 1098 ATC 1152 TTG	GTG V CTT L AAA	CTC L CGA R CTT	999 AAC N 1053 -CTT L 1107 1161 AGT 1215	P CCA P TTC	L ATT	1008 GTC V 1062 GTG V 1116 TCA 1170 3 AAA	TAT Y GCC A GAG	GGA G ACA T TCC	1017 GTG V 1071 CAC H 1125 TCT 1179	AAG K GCT A GAT	ACA T TCA S TCA AAT	1026 AAG
GAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG 	CAG Q GTCA	CCT P CGC R	990 CCT P 1044 ATC 1098 ATC 1152 TTG	GTG V CTT L AAA	CTC L CGA R CTT R AAT	999 AAC N 1053 -CTT L 1107 1161 1215	P CCA P TTC	L ATT	1008 GTC V 1062 GTG V 1116 TCA 1224 GTT 1224	TAT Y GCC A GAG	GGA G ACA T TCC	1017 GTG V 1071 CAC H 1125 TCT 1233 TCT	AAG K GCT A GAT	ACA T TCA S TCA TCA TTA	1026 AAG K 1080 GAG E 1134 GAT 1188 AAA 1242 TTT 1296
GAG GAG CCC P	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG 	GTT V CAG	CCT P CGC R GTG GTG GTG GTG GTG GTG GTG GTG GTG G	990 CCT P 1044 ATC 1098 ATC 1152 TTG 1206	GTG V CTT L AAA	CTC L CGA R CTT	999 AAC N 1053 CTT L 1107 CTT 1161 AGT 1215 AGT 1269	P CCA P TTC F TTC	CAT CAT CAT CAT CAT CAG	1008 GTC V 1062 GTG V 1116 TCA 1224 GTT 1278	TAT Y GCC A GAG	GGA G ACA T TCC	1017 GTG V 1071 CAC H 1125 TCT 1233 TCT 1287	AAG K GCT A GAT CTT CCA	ACA T TCA S TCA AAT	1026 AAG K 1080 GAG E 1134 GAT 1188 AAA 1242 TTT 1296 GAC
GAG GAG CCC P	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG 1197 AAC	CAG Q GTCA GTCA	CCT P CGC R GTG	1098 ATC	GTG V CTT L GAA	CTC L CGA R CTT R TTT	999 AAC N 1053 CTT L 1161 AGT 1215 ATG	P CCA P TTC F TTC	CAT	1008 GTC V 1062 GTG V 1116 TCA 1224 GTT 1278	TAT Y GCC A GAG	GGA G ACA T TCC	1017 GTG V 1071 CAC H 1125 TCT 1233 TCT 1287	AAG K GCT A GAT CTT CCA	ACA T TCA S TCA AAT	1026 AAG K 1080 GAG E 1134 GAT 1188 AAA 1242 TTT 1296 GAC
GAG GAG CCC P	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG 1197 AAC	CAG Q GTCA GTCA	CCT P CGC R GTG	1098 ATC	GTG V CTT L GAA	CTC L CGA R CTT R TTT	999 AAC N 1053 CTT L 1161 AGT 1215 ATG	P CCA P TTC F TTC	CAT	1008 GTC V 1062 GTG V 1116 TCA 1224 GTT 1278	TAT Y GCC A GAG	GGA G ACA T TCC	1017 GTG V 1071 CAC H 1125 TCT 1233 TCT 1287	AAG K GCT A GAT CCA TAC	ACA T TCA S TCA AAT	1026 AAG K 1080 GAG E 1134 GAT 1188 AAA 1242 TTT 1296
GAG GAG CCC P TTT AAA	CTG L ATT I TAG	981 CTG L 1035 CGA R 1089 GTG 1197 AAC	CAG Q GTCA GTCA	CCT P CGC R GTG	1098 ATC 1098 ATC 1206 CTT	GTG V CTT L GAA	CTC L CGA R CTT R TTT	999 AAC N 1053 CTT L 1161 AGT 1215 ATG 1269	P CCA P TTC F TTC	CAT	1008 GTC V 1062 GTG V 1116 TCA 1224 GTT 1278 1783	TAT Y GCC A GAG	GGA G ACA T TCC	1017 GTG V 1071 CAC H 1125 TCT 1233 TCT 1287	AAG K GCT A GAT	ACA T TCA S TCA AAT	1026 AAG K 1080 GAG E 1134 GAT 1188 AAA 1242 TTT 1296 GAC

FIG. 2C

																	*,
	135	9		136	8		1377	7	7 1	1386	5		1395	5		1404	
AA	C TG	C TT	C TAC	C TG	A TGC	: TTI	' ACA	\ GC	A TTC	TG	A GAT	י אאר	י בב	car	ר אכיא	Tr.Com	303
																	
		141	3		1422	2		1437	ı		1440	1		7440	3		7.450
GA.	A CA	T TT	G CCI	A AAC	G GCC	TAD	GCA	CGG	- 2 CA2	A A C C	י אא ב	, , , , , , , , , , , , , , , , , , , ,	330	733;	,		1458
						- 151	. GCA	· CGC	5 CAA	AGG	* AAA	ATF	AAC	ACA	A GAA	TAT	AAT
		146	7		1476				- 		- 						
277		770	7		14/0			1485			1494	Ŀ		1503	3		1512
MAA	. AI	J AG.	A TA	A TC	r AGC	TTA	AAA	CT	A TAA	CTI	CCI	CTT	CAG	AAC	TCC	CAA	CCA
										·					 -		
		152	1		1530			1539)		1548	3		1557	7		1566
CAT	TG	3 AT	C TCF	A GAZ	AAA /	TGC	TGT	CTI	CAA	TAA	. GPC	' ጥጥር	ጥአር	י ארי	(222	733	
		157	5		1584			1593	:		1602			1611			1620
ATI	TT	CC	r CTC	GAC	ACT	AGC	ACT	TAB	GGG	. GAA	CAT	TOO	330	ת מידי		- amm	1020
											. GAI	100	ANG	IAA	AGC	CIT	GAA
		1629	9		1638			1647			1656						
220	. AC	ים ארי		300		amm		104/			T020			T002)		1674
		. AC	A TTI	ACC	. IAC	GIT	AAT	GAA	AGT	TGA	CAC	ACT	GTT	CTG	AGA	GTT	TTC
		160															
		798	3		1692			1701			1710			1719			1728
ACA	. GC	I TA	. GGA	CCC	TGT	TTTT	TCC	ጥልጥ	מידידי י	ידיידי ב	444	THE PARTY IN	TT CON	300	~~~		
		1737	,		1746			1755			1764			1772		-	700
GGC	AA	GA1	TTA :	' ATT	' AGT	ACC	CTC	ATT	GTA	GCC	ATG	CCA	222	TTC	ATC	TOTAL	3 Cm
		- - -															AGI
		1791	-		1800			POST			1010						
GGG	GAT	CAC	TGA	ירידע	444	TCC	COT	Cam	3.03	3.0m	70T0			102/			L836
					, mun	100	GGI	CAI	ACA	AGI	ATA	AAA	ATT	AAA	AAA	AAA	AAA
		1845			7054												
a. a	mm.				1854		-	1863			1872			1881		1	.890
GAC	TTC	ATG		AA'I'	CIC	ATA	TGA	TGT	GGA	AGA	አ ርጥ	CTTT	מכות	CAC	300	330	300
		1899			1908		1	1917		•	1926		-	1935		-	011
GTA	GTG	GGT	' TAG	AGA	TTT	CCA	GAG	TOT	ጥልሮ	ልጥጥ	ጥጥር	ጥአር	300	300	m a m		
		1953			1962		3	971			1980			000			
TCT	TCT	CAC	TCA	TCC	AGT	CTT	GT N	TT.C.	300	220		0000		1909		T	998
					2101	GII	GIA	111	AGG	WYI	TIC	CTG	GCA	ACA	GAA	CTC	ATG
		2007			2016												
a a m	mm 3	2007			2016		2	2025		2	2034		2	043		2	052
GCI	TTA	ATC	CCA	CTA	GCT	ATT	GCT	TAT	TGT	CCT	GGT	CCA	ATT	GCC	AAT	TAC	CTG
		2061		:	2070		2	079		- 2	8809		2	097		2	106
TGT	CTT	GGA	AGA	AGT	GAT	TTC	TAG	GTT	CAC	CAT	ጥልጥ	CCA	A C A	ጥጥረ	ጥጥአ	TTTC	202
		2115	ምአ ር		2124		2	133		2	142		2	151			
AAG	TCT	GCA	TAG	GGC	TTA	ጥልር	מא א	CTT	A TITT	mam -	. A.Z.A			TOT			T 2 O
						ING	CAA	GII	AII	IMI	111	TAA	AAG	TTC	CAT	AGG '	TGA
		2160			170												
		4109			17.18		2	187		2	196		2	205		2:	214
TTC	TGA	TAG	GCA	GTG	AGG	TTA	GGG	AGC	CAC	CAG	TTA	TGA	TGG	GAA	GTA	TGG 2	AAT
	:	2223		2	232		2	241		2	250		2	259		2.	268
GGC	AGG	TCT	TGA	AGA	TAA	CAT	TGG	CCT	TTT	GAG	TGT	CAC	TCG	ጥልር	CTC	GAA :	A (7)
															-16	JAM A	rG1
		2277		2	286		- -	295	-		204						
GAG				300	7.00	3 m/r		473 ma∞	mm	2	304		2	313		23	322
	JUN	AIC	TTC	AGG	ACC.	MIG	CIT	TAT	T.I.C	GGG	CTT	TGT	GCA	GTA	TGG .	AAC 1	AGG
		2331		2	340		2	349		2	358		2	367		23	376
GAC	TTT	GAG	ACC	AGG	AAA (GCA.	ATC :	TGA	CTT .	AGG۱	CAT	GGG .	AAT	CAG	GCA '	TTT 7	TG
																	•

FIG. 2D

					4												
CTT	CTG	AGG	GGC	TAT	TAC							ATC	TTC	AAC	AGG	ATA	TGA
	_	439			2448												
CAA	CAG	TGT	TAA											ATG	TGA	TCA	TAT
					2502												2538
	TGG																TCC
		547			2556												
	AAC																TAT
	_	601			2610												
TTA	ATA															TAT	TAT
	_	655			2664												
TGA	ATG	TCA	TCT	CTG	TTC	ATC	ATT	GAC	TGC	TCT	TTG	CTC	ATC	ATT	GAA	TCC	CCC
	_	709			2718									_		_	2754
AGC	AAA	GTG													ATT		
					- 												
	_	763			2772												808
CAA	ACC	TGA	TTC														
mma	_	817			2826												
TTG	AGT				TTA			GGC									TGA
~~					2880												
CAT	GTG	CAA	TTT	CTA	TAC	CTG	GCT	CAT	AAA	ACC	CTC	CCA	TGT	GCA	GCC	TTT	CAT
		925		,	2934		,			,	2052		,				
O TO TO	GAC .																
GII	GAC .	ALL	MAA		GAC												
		979			2988												
330	CCT		tronor.	ama	333		ama	4991 maa	202	000	3000	0.CI		DOTO	mmm		3024
AAG	CCT	GGA	TTT	CIG	AAA	AAA		TGC									
		033			3042												
000	_															_	
CCC	ACT '	TGT.		TGT				TTG					ATA			TAT	TGT
		097	_		3096											,	
GTC.	AAG				-					_			_			-	
GIC	ANG .	nnn	AAA.	AAA	www	AAA		MMA	www	AAA	WWW	HAA	MAA	AAA	MAM	AAA	AAA

AAA A 3'

Figure 3: Protein Sequence for 101P3A11 (piece of SEQ IN M: 2880)

MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDILI STSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHATVLTLPRVTKIGV AAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYL LILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYG VKTKEIRQRILRLFHVATHASEP

Figure 4

Alignment of 101P3A11 (Sbjct) with mouse olfactory receptor S25 (Query)

- Query: 34 GNYTVVTEFILLGLTDDITVSVILFVMFLIVYSVTLMGNLNIIVLIRTSPQLHTPMYLFL 93
 GN + T FIL+GL L +Y + ++GNL II ++RT LH PMY+FL
- Sbjct: 6 GNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL 65
- Query: 94 SHLAFLDIGYSSSVTPIMLRGFLRKGTFIPVAGCVAQLCIVVAFGTSESFLLASMAYDRY 153
- L+ +DI S+S P ML F T I C+ Q+ + + ES +L +MA+DRY
- Sbjct: 66 CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRY 125
- Query: 154 VAICSPLLYSTQMSSTVC1LLVGTSYLGGWVNAWIFTGCSLNLSFCGPNKINHFFCDYSP 213
 VAIC PL ++T ++ + + + G L FC N ++H +C +
- Sbjct: 126 VAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQD 185
- Query: 214 LLKLSCSHDFSFEVIPAISSGSIIVVTVFIIALSYVYILVSILKMRSTEGRQKAFSTCTS 273
- ++KL+C V I S I + +I+ SY+ IL ++L + + E + KAF TC S Sbjct: 186 VMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 244
- Query: 274 HLTAVTLFFGTITFIYVMPQSSYSTDQNK----VVSVFYTVVIPMLNPLIYSFRNKEVKE 329
- H+ AV +F+ + FI + +S ++ +++ Y +V P+LNP++Y + KE+++
- Sbjct: 245 HVCAVFIFY--VPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQ 302

Query: 330 AMKKL 334 (SEQ IS NO: 2881)

+ +L Sbjct: 303 RILRL 307 (SEQ In No: 2822)

Figure 23: Alignment of 101P3A11-PHOR-1 with the rat GPCR RA1C (gi|3420759).

Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%)

- PHOR: 14 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73 F+LIG+PGLEEA FW FPL S+Y +A+ GN +++IVRTE SLH PMY+FLCML+ ID+
- RAIC: 11 FMLIGIPGLEEAHFWFGFPLLSMYAVALFGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70
- PHOR: 74 LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133 +STS+MPK+LA+FWF+S I FDACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
- RAIC: 71 ALSTSTMPKILALFWFDSREITFDACLAQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130
- PHOR: 134 HATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
 HA VL +IG+ A+VRG+ PLP+ IK+L FC SN+LSHSYC+HQDVMKLA D
- RAIC: 131 HAAVLNNTVTVQIGMVALVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYTD 190
- PHOR: 194 IRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252 NVVYGL I+ +G+D + IS SY LI++ VL L ++ +AKAFGTCVSH+ V F
- RA1C: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRAVLQLPSKSERAKAFGTCVSHIGVVLAF 250
- PHOR: 253 YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311 (EQ TP M: 1223)
- YVP IGLS+VHRF D + V++ ++YLL+PPV+NPI+YG KTK+IR R+L +F ++
 RAIC: 251 YVPLIGLSVVHRFGNSLDPIVHVLMGDVYLLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309 (XEQ ID NO: 2274)

Figure 24: Alignment of 101P3All-PHOR-1 with the human prostate specific GPCR.(gi|13540539)

Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%)

- PHOR: 14 FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
 F+LIG+PGLE+A FW+ FPL S+Y++A+ GN +++IVRTE SLH PMY+FLCML+ ID+
- GPCR: 11 FVLIGIPGLEKAHFWVGFPLLSMYVVAMFGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70
- PHOR: 74 LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133 +STS+MPK+LA+FWF+S I F+ACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
- GPCR: 71 ALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130
- PHOR: 134 HATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
- HA VL +IG+ AVVRG+ PLP+ IK+L FC SN+LSHSYC+HQDVMKLA D
 GPCR: 131 HAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYAD 190
- PHOR: 194 IRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
- NVVYGL I+ +G+D + IS SY LI++TVL L ++ +AKAFGTCVSH+ V F GPCR: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAF 250
- PHOR: 253 YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311 (SEQ 18 M: 2885)
- YVP IGLS+VHRF + V++ +IYLL+PPV+NPI+YG KTK+IR R+L +F ++
 GPCR: 251 YVPLIGLSVVHRFGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309 (SEQ IN M: 2886)

Figure 25: Alignment with human olfactory receptor 5II12 (gi|14423836)

Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%)

- PHOR: 7 NESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLC 66 N + +F+L G+PGLE + WL+ PLC +Y +A+ GN I+ VR E SLHEPMY FL
- HOR5: 5 NVTHPAFFLLTGIPGLESSHSWLSGPLCVMYAVALGGNTVILQAVRVEPSLHEPMYYFLS 64
- PHOR: 67 MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126 MLS D+ IS +++P +L F N+ I FDACL+Q+F IH S MES +LLAM+FDRYV
- HOR5: 65 MLSFSDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYV 124
- PHOR: 127 AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 186
 AIC PLR+ATVLT + +G+ A R + PLP IK+LP CRSN+LSHSYCLH D+
- HOR5: 125 AICDPLRYATVLTTEVIAAMGLGAAARSFITLFPLPFLIKRLPICRSNVLSHSYCLHPDM 184
- PHOR: 187 MKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH 245
- M+LAC DI +N +YGL V++S G+D I SY+LIL++V+ +RE + KA TCVSH HOR5: 185 MRLACADISINSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSH 244
- PHOR: 246 VCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRIL 305
- + AV FYVP IG+S VHRF K + V+++N+YL VPPVLNP++Y KTKEIR+ I HOR5: 245 ILAVLAFYVPMIGVSTVHRFGKHVPCYIHVLMSNVYLFVPPVLNPLIYSAKTKEIRRAIF 304
- PHOR: 306 RLFH 309 (SEQ 370 NO: 2887)
- HORS: 305 RMFH 308 (SEQ TR NO: 2888)